Search History

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OM protein - protein search, using sw model

                                    GenCore version 5.1.7
                                    Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:          May  4, 2006, 05:25:14 ; Search time 28.6667 Seconds
                                    (without alignments)
                                    902.703 Million cell updates/sec

Title:           US-10-705-757-2
Perfect score:   1670
Sequence:        1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:   572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
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                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1670	100.0	313	2	US-10-705-757-2	Sequence 2, Appli
2	1670	100.0	313	2	US-09-237-543-9	Sequence 9, Appli
3	1657	99.2	313	1	US-09-644-450-9	Sequence 9, Appli
4	1657	99.2	313	1	US-08-463-081B-26	Sequence 26, Appli
5	1657	99.2	313	1	US-08-462-379A-26	Sequence 26, Appli
6	1657	99.2	313	1	US-08-462-390B-26	Sequence 26, Appli
7	1657	99.2	313	2	US-08-463-074B-26	Sequence 26, Appli
8	1657	99.2	313	2	US-08-465-585C-26	Sequence 26, Appli
9	1636	98.0	313	2	US-08-652-446-26	Sequence 26, Appli
10	1636	98.0	313	2	US-09-237-543-8	Sequence 8, Appl
11	1582	94.7	313	2	US-09-644-450-8	Sequence 8, Appl
12	1582	94.7	313	2	US-09-237-543-7	Sequence 7, Appl
13	1296.5	77.6	257	1	US-09-644-450-7	Sequence 7, Appl
14	1133	67.8	326	2	US-07-857-224B-41	Sequence 41, Appl
15	1133	67.8	326	2	US-09-237-543-2	Sequence 2, Appl
16	1128.5	67.6	455	2	US-09-237-543-5	Sequence 5, Appl
17	1128.5	67.6	455	2	US-09-644-450-5	Sequence 5, Appli
18	1105	66.2	323	2	US-09-237-543-6	Sequence 6, Appli
19	1105	66.2	323	2	US-09-644-450-6	Sequence 6, Appli
20	1079.5	64.6	254	2	US-09-237-543-4	Sequence 4, Appli
21	1079.5	64.6	254	2	US-09-644-450-4	Sequence 4, Appli
22	869.5	52.1	311	2	US-10-184-563-2	Sequence 2, Appli
23	869.5	52.1	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	384.5	23.0	256	2	US-09-964-956-74	Sequence 74, Appl
25	376.5	22.5	776	2	US-09-523-849-34	Sequence 34, Appl
26	376	22.5	1101	2	US-09-770-170-8	Sequence 8, Appli
27	370.5	22.2	778	2	US-10-116-326-2	Sequence 2, Appli
28	370.5	22.2	778	2	US-10-003-690-2	Sequence 2, Appli
29	370.5	22.2	778	2	US-10-803-277-2	Sequence 2, Appl
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31	368.5	22.1	631	2	US-09-579-664B-11	Sequence 11, Appl
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33	367	22.0	1356	2	US-09-770-170-6	Sequence 6, Appli
34	364.5	21.8	256	2	US-09-964-956-72	Sequence 72, Appl
35	362.5	21.7	1323	2	US-09-770-170-2	Sequence 2, Appli
36	359	21.5	511	2	US-09-633-328B-4	Sequence 4, Appli
37	358.5	21.5	281	2	US-09-248-796A-20512	Sequence 20512, A
38	358.5	21.5	668	2	US-10-930-181-2	Sequence 2, Appli
39	357.5	21.4	674	2	US-10-054-579-2	Sequence 2, Appli
40	357.5	21.4	674	2	US-10-283-247-2	Sequence 2, Appli
41	357	21.4	512	2	US-09-633-328B-2	Sequence 2, Appli
42	353.5	21.2	674	2	US-10-283-247-7	Sequence 7, Appli
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44	349.5	20.9	722	2	US-10-817-832B-32	Sequence 32, Appl
45	348.5	20.9	722	2	US-09-984-890-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-237-543-9
; Sequence 9, Application US/0923754 3A
; Patent No. 6143540
; GENERAL INFORMATION:
;  APPLICANT: Kapeller, Rosana
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 035800/175631
;  CURRENT APPLICATION NUMBER: US/09/237,543A
;  CURRENT FILING DATE: 1999-01-26
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
;
;  SEQ ID NO 9
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-237-543-9

Query Match             100.0%;  Score 1670;  DB 2;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 7.5e-161;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy      61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Qy     121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy     181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Qy     241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Qy     301 EIHLHSLSPGPSK 313
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RESULT 2
US-09-644-450-9
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; Sequence 9, Application US/09644450
; GENERAL INFORMATION:
; Patent No. 6383791
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-9

Query Match   100.0%; Score 1670; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.5e-161;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 3
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; GENERAL INFORMATION:
; Patent No. 5871960 5837487
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-081B-26

Query Match   99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db  301 EIHLHSLSPGPSK 313
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RESULT 4
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; Patent No. 5871961
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.25
; SOFTWARE: Version #1.0,

CURRENT APPLICATION DATA:
~ APPLICATION NUMBER: US/08/461,379A
~ FILING DATE: 5-JUNE-1995
~ PRIOR APPLICATION DATA:
~ APPLICATION NUMBER: USSN 08/330,108; 08/104,736
~ FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
~ APPLICATION NUMBER: & 07/796,066
~ FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
~ ATTORNEY/AGENT INFORMATION:
~ NAME: Viviana Amzel, Ph. D.
~ REGISTRATION NUMBER: 30,930
~ REFERENCE/DOCKET NUMBER: DART-070
~ TELECOMMUNICATION INFORMATION:
~ TELEPHONE: (610)470-0701
~ TELEFAX: (610)470-0700
~ INFORMATION FOR SEQ ID NO: 26:
~ SEQUENCE CHARACTERISTICS:
~ LENGTH: 313 amino acids
~ TYPE: peptide
~ STRANDEDNESS: n.a.
~ TOPOLOGY: n.a.
~ MOLECULE TYPE: peptide
~ US-08-461-379A-26

Query Match 99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 5
US-08-462-390B-26
; Sequence 26, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
~ APPLICATION NUMBER: US/08/462,390B
~ FILING DATE: 5-JUNE-1995
~ PRIOR APPLICATION DATA:
~ APPLICATION NUMBER: USSN 08/330,108
~ FILING DATE: 27-OCT-1994
~ APPLICATION NUMBER: USSN 08/104,736
~ FILING DATE: 10-AUG-1993
~ APPLICATION NUMBER: USSN 07/796,066
~ FILING DATE: 20-NOV-91
~ ATTORNEY/AGENT INFORMATION:
~ NAME: Viviana Amzel, Ph. D.
~ REGISTRATION NUMBER: 30,930
~ REFERENCE/DOCKET NUMBER: DART-040
~ TELECOMMUNICATION INFORMATION:
~ TELEPHONE: (610)407-0701
~ TELEFAX: (610)407-0700
~ INFORMATION FOR SEQ ID NO: 26:
~ SEQUENCE CHARACTERISTICS:
~ LENGTH: 313 amino acids
~ TYPE: peptide
~ STRANDEDNESS: n.a.
~ TOPOLOGY: n.a.
~ MOLECULE TYPE: peptide
~ US-08-462-390B-26

Query Match 99.2%; Score 1657; DB 1; Length 313;
Best Local Similarity 99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  301 EIHLHSLSPGPSK 313
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RESULT 6
US-08-463-074B-26
; Sequence 26, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 190
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

RESULT 7
US-08-465-585C-26
Sequence 26, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
 APPLICANT: Smith, K. A.; & Beadling, C.
 TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  (B) STREET: 444South Flower St. - Suite 190
  CITY: Los Angeles
  STATE: California
  COUNTRY: USA
  ZIP: 900071

; .
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,074B
; PRIOR APPLICATION DATA:
; FILING DATE: 5-JUN-1995
; APPLICATION NUMBER: US 08/104,736
; PRIOR APPLICATION DATA:
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: peptide
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-074B-26

Query Match   99.2%; Score 1657; DB 2; Length 313;
Best Local Similarity   99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 8
US-08-652-446-26
Sequence 26, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
 APPLICANT: Smith, Kendall A. & Beadling, Carol
 TITLE OF INVENTION: Nucleic Acids Encoding CR5
 TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
 TITLE OF INVENTION: Expression Thereof
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  (B) STREET: 444 South Flower St. - Suite 1900
  ADDRESSEE:

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,585C
; PRIOR APPLICATION DATA:
; FILING DATE: 5-JUNE-1995
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 4894210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: peptide
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-465-585C-26

Query Match   99.2%; Score 1657; DB 2; Length 313;
Best Local Similarity   99.4%; Pred. No. 1.6e-159;
Matches 311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

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;     CITY:  Los Angeles
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  90071
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0,
;     SOFTWARE:  Version #1.25
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/652,446
;     FILING DATE:
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  EP App. # 96921319.8
;     FILING DATE:  5-JAN-1998
;     APPLICATION NUMBER:  PCT/US/96/09194
;     FILING DATE:  5-JUN-1996
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/330,108
;     FILING DATE:  27-OCT-1994
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/463,074
;     FILING DATE:  5-JUN-1995
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/462,337
;     FILING DATE:  5-JUN-1995
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/462,390
;     FILING DATE:  5-JUN-1995
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/465,585
;     FILING DATE:  5-JUN-1995
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/461,379
;     FILING DATE:  5-JUN-1991
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/463,081
;     FILING DATE:  5-JUN-1991
;     APPLICATION NUMBER:  08/739,523
;     FILING DATE:  29-OCT-1996
;  ATTORNEY/AGENT INFORMATION:
;     NAME:  Viviana Amzel, Ph. D.
;     REGISTRATION NUMBER:  30,930
;     REFERENCE/DOCKET NUMBER:  FP66 40035
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (213) 622-7700
;     TELEFAX:  (213) 489-4210
;  INFORMATION FOR SEQ ID NO: 26:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH:  313 amino acids
;     TYPE:  peptide
;     STRANDEDNESS:  n.a.
;     TOPOLOGY:  n.a.
;     MOLECULE TYPE:  peptide

Query Match             99.2%;  Score 1657;  DB 2;  Length 313;
Best Local Similarity   99.4%;  Pred. No. 1.6e-159;
Matches   311;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60
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Db      1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
            |||||||||||||
Db    301 EIHLHSLSPGPSK 313


RESULT 9
US-09-237-543-8
; Sequence 8, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION:  NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   SOFTWARE: PatentIn Ver. 2.0
;   NUMBER OF SEQ ID NOS: 11
;   SEQ ID NO 8
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match             98.0%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 2.1e-157;
Matches   304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

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Db      1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
            ||||||||: |||||||||||||||||||||:|||||||:||||||||||||||||| ||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
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Db    301 EIHLHSLSPGPSK 313


RESULT 10
US-09-644-450-8
; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION:  NOVEL MOLECULES
;   TITLE OF INVENTION:  AND USES THEREOF
;   TITLE OF INVENTION:  OF THE HKID-1-RELATED PROTEIN FAMILY
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
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;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 8
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match             98.0%;  Score 1636;  DB 2;  Length 313;
Best Local Similarity   97.1%;
  Matches  304;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFSGVYSGIRVSD 60
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Db          1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFSGVYSGIRVAD 60

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Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db        241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy        301 EIHLHSLSPGPSK 313
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Db        301 EIHLHSLSPGSSK 313


RESULT 11
US-09-237-543-7
;   Sequence 7, Application US/09237543A
;   Patent No. 6143540
;   GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 7
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-237-543-7

Query Match             94.7%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity   93.9%;
  Matches  294;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

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Db          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFSGVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

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Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQDLLPQAAS 300

Qy        301 EIHLHSLSPGPSK 313
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Db        181 EIKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

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Qy        301 EIHLHSLSPGPSK 313
Db        301 EIHLHSLSPGSSK 313


RESULT 12
US-09-644-450-7
;   Sequence 7, Application US/09644450
;   Patent No. 6387791
;   GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 7
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-644-450-7

Query Match             94.7%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity   93.9%;
  Matches  294;  Conservative   10;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFSGVYSGIRVSD 60
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Db        181 EIKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIRNHPWMQDLLPQAAS 300

Qy        301 EIHLHSLSPGPSK 313
Db        301 EIHLHSLSPGSSK 313


RESULT 13
US-07-857-224B-41
;   Sequence 41, Application US/078572248
;   Patent No. 5958784
;   GENERAL INFORMATION:
;   APPLICANT: Benner, Steven A.
;   TITLE OF INVENTION: Predicting Folded Structures of Proteins
;   NUMBER OF SEQUENCES: 114
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Steven A. Benner
;   STREET: Hadlaubstrasse 151
;   CITY: Zurich
;   STATE: none
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;     COUNTRY: Switzerland
;     ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;     COMPUTER: Apple Macintosh
;     OPERATING SYSTEM: Macintosh 7.0
;     SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07,857,224B
;     FILING DATE: 03/25/92
; PRIOR APPLICATION DATA:
;     CLASSIFICATION: 436
;     APPLICATION: none
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (international) 41 1 632 2830
;     TELEFAX: (international) 41 1 262 2437
;     TELEX: none
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 257
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE:
;     DESCRIPTION: protein
; ORIGINAL SOURCE:
;     ORGANISM: rat
; FEATURE: Protein kinase; Table 8 Column 46
; PUBLICATION INFORMATION:
;     AUTHORS:
;     AUTHORS: Hanks, S. K.
;     AUTHORS: Quinn, A. M.
;     AUTHORS: Hunter, T.
;     TITLE: The protein kinase family
;     JOURNAL: Science
;     VOLUME: 241
;     PAGES: 42-52
;     DATE: 1988
US-07-857-224B-41

Query Match             77.6%;  Score 1296.5; DB 1; Length 257;
Best Local Similarity   94.2%;  Pred. No. 4.1e-123;
Matches 242; Conservative   9; Mismatches   3; Indels   3; Gaps   2;

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Db     1 SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVPMEVVLLKK  58

Qy    96 VSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAV 155
         ||| ||||||||||||||||:|||||||||||||||||||||||||:|||||||||||||
Db    59 VSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAV 118

Qy   116 RHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY 175
         |||||||||||||||||||:|||||||||||||||||||||:|||||||||||||||||
Db   119 RHCHNCGVLHRDIKDENILIDLSRGEIKLIIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY 178

Qy   216 HRYHGRSAAVWSLGILLYDMYCGDIPF-EHDEEIIRGQVFRQRVSSECQHLIRWCLALR 274
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Db   179 HRYHGRSAAVWSLGILLYDMVCGDIPFDEHDEEIIKGQVFRQTVSSECQHLIKWCLSLR 238

Qy   275 PSDRPTFEEIQNHPWMQ 291
         ||||||||:||||||||
Db   239 PSDRPSFEEIRNHPWMQ 255

RESULT 14
US-09-237-543-2
; Sequence 2, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 03580D/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
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; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;     LENGTH: 326
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-09-237-543-2

Query Match             67.8%;  Score 1133; DB 2; Length 326;
Best Local Similarity   69.3%;  Pred. No. 2.1e-106;
Matches 219; Conservative  35; Mismatches  52; Indels  10; Gaps   7;

Qy     1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
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Db     1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGPLLGSGGFGSVYSGIR  59

Qy    58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         ::|||||||||||||||:|||||||||||||||||||||  ||||||||||||||||||
Db    60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy   116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         |||||||||||||||||||||||||:|||||||||||||||||:||||||||||||||||
Db   119 FVLILERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENILV 178

Qy   176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
         || ||||:||||||||:|:|||||||||||||||||||||||||||||||||||||||||
Db   179 DLRSGELKLIIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEEHDEEIIRGQVFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
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Db   239 VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298

Qy   294 LLPQETAEIHLHSLSP 309
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Db   299 GAP-ESCDLRLCTLDP 313

RESULT 15
US-09-644-450-2
; Sequence 2, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 03580D/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;     LENGTH: 326
;     TYPE: PRT
;     ORGANISM: Homo sapiens
US-09-644-450-2

Query Match             67.8%;  Score 1133; DB 2; Length 326;
Best Local Similarity   69.3%;  Pred. No. 2.1e-106;
Matches 219; Conservative  35; Mismatches  52; Indels  10; Gaps   7;

Qy     1 MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
         |||||     |  :|||  ::|| | |:| ||  || |||||||||||||||||||||||
Db     1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGPLLGSGGFGTVYAGSR  59

Qy    58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         ::|||||||||||||||:|||||||||||||||||||||  ||||||||||||||||||
Db    60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy   116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         |||||||||||||||||||||||||:|||||||||||||||||:||||||||||||||||
Db   119 FVLILERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENILV 178
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Qy   176 DLNRGELKLIDFGSGGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
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Db   179 DLRSGELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
             ||||||||:||||:||:| ||:::| ::|||||::||| ||| : ::: |||||   ||
Db   239 VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298

Qy   294 LLPQETAEIHLHSLSP 309
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Db   299 GAP-ESCDLRLCTLDP 313
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Search completed: May 4, 2006, 05:27:21
Job time : 29.6667 secs

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: May 4, 2006, 05:26:13 ; Search time 92.6667 Seconds
                                        (without alignments)
                                        1411.301 Million cell updates/sec

Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA_Main:*
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                2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	313	3	US-09-971-791-9	Sequence 9, Appli
2	1670	100.0	313	4	US-10-081-119-18	Sequence 18, Appl
3	1670	100.0	313	4	US-10-394-332A-52	Sequence 52, Appli
4	1670	100.0	313	4	US-10-348-081-13	Sequence 13, Appl
5	1670	100.0	313	4	US-10-664-421-1	Sequence 1, Appli
6	1670	100.0	313	4	US-10-664-421-150	Sequence 150, App
7	1670	100.0	313	4	US-10-705-757-2	Sequence 2, Appli
8	1670	100.0	313	4	US-10-377-268-9	Sequence 9, Appli
9	1670	100.0	313	5	US-10-951-389-18	Sequence 18, Appl
10	1670	100.0	313	5	US-10-951-406-18	Sequence 18, Appl
11	1670	100.0	313	5	US-10-951-477-18	Sequence 18, Appl
12	1670	100.0	313	5	US-10-977-087-18	Sequence 18, Appl
13	1670	100.0	313	5	US-10-941-635-1	Sequence 1, Appli
14	1670	100.0	313	5	US-10-941-635-152	Sequence 152, App
15	1657	99.2	313	4	US-10-620-05A-22	Sequence 22, Appl
16	1636	98.0	313	3	US-09-971-791-8	Sequence 8, Appli
17	1636	98.0	313	4	US-10-348-081-12	Sequence 12, Appl
18	1636	98.0	313	4	US-10-705-757-4	Sequence 4, Appli
19	1582	94.7	313	3	US-09-971-791-7	Sequence 7, Appli
20	1582	94.7	313	4	US-10-348-081-14	Sequence 14, Appl
21	1582	94.7	313	4	US-10-664-421-2	Sequence 2, Appli
22	1582	94.7	313	4	US-10-705-757-6	Sequence 6, Appli
23	1582	94.7	313	4	US-10-377-268-10	Sequence 10, Appl
24	1582	94.7	313	5	US-10-941-635-2	Sequence 2, Appli
25	1362	81.6	253	4	US-10-620-052A-71	Sequence 71, Appl
26	1140	68.3	323	4	US-10-664-421-7	Sequence 7, Appli
27	1140	68.3	323	4	US-10-377-268-15	Sequence 15, Appl
28	1140	68.3	323	5	US-10-941-635-7	Sequence 7, Appli
29	1135	68.0	374	3	US-10-425-114-54275	Sequence 54275, A
30	1133	67.8	326	3	US-09-971-791-2	Sequence 2, Appli
31	1133	67.8	326	4	US-10-348-081-2	Sequence 2, Appli
32	1133	67.8	326	4	US-10-664-421-166	Sequence 166, App
33	1133	67.8	326	4	US-10-618-941-82	Sequence 82, Appl
34	1133	67.8	374	3	US-10-425-114-54264	Sequence 54264, A
35	1129.5	67.6	326	4	US-10-348-081-6	Sequence 6, Appli
36	1129.5	67.6	326	4	US-10-705-757-11	Sequence 11, Appl
37	1129.5	67.6	326	4	US-10-377-268-14	Sequence 14, Appl
38	1129.5	67.6	326	4	US-10-941-635-6	Sequence 6, Appli
39	1128.5	67.6	326	4	US-10-348-081-10	Sequence 10, Appl
40	1128.5	67.6	455	3	US-09-971-791-5	Sequence 5, Appli
41	1128.5	67.6	455	4	US-10-705-757-9	Sequence 9, Appli
42	1116	66.8	325	4	US-10-664-421-6	Sequence 6, Appli
43	1105	66.2	323	3	US-09-971-791-6	Sequence 6, Appli
44	1105	66.2	323	4	US-10-348-081-11	Sequence 11, Appli
45	1105	66.2	323	4	US-10-664-421-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US2002011520A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES T?
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9

Query Match   100.0%;   Score 1670;   DB 3;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 2.2e-143;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
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Db        301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 2
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313

; ORGANISM: Homo sapiens
US-10-394-322A-52

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 3
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT

RESULT 4
US-10-348-081-13
; Sequence 13, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13

Query Match   100.0%; Score 1670; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

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Qy   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
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Db   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy   301  EIHLHSLSPGPSK  313
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Db   301  EIHLHSLSPGPSK  313
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RESULT 5
US-10-664-421-1
Sequence 1, Application US/10664421
Publication No. US20040142864A1

GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 3.2
;
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-1

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Query Match            100.0%;  Score 1670;  DB 4;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 2.2e-143;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180

Qy   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy   301  EIHLHSLSPGPSK  313
          |||||||||||||
Db   301  EIHLHSLSPGPSK  313
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RESULT 6
US-10-664-421-150
Sequence 150, Application US/10664421
Publication No. US20040142864A1

GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 3.2
;
; SEQ ID NO 150
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-150

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Query Match            100.0%;  Score 1670;  DB 4;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 2.2e-143;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
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RESULT 7
US-10-705-757-2
Sequence 2, Application US/10705757
Publication No. US20040146942A1

GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-757-2

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Query Match            100.0%;  Score 1670;  DB 4;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 2.2e-143;
Matches  313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180

Qy   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy   301  EIHLHSLSPGPSK  313
          |||||||||||||
Db   301  EIHLHSLSPGPSK  313
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Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60
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RESULT 8
US-10-377-268-9

; Sequence 9, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9

Query Match   100.0%;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Score 1670; DB 4; Length 313;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 9
US-10-951-389-18

; Sequence 18, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Chan, Vivien W.
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-18

Query Match   100.0%;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Score 1670; DB 5; Length 313;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313
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RESULT 10
US-10-951-406-18

; Sequence 18, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Chan, Vivien W.
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406

; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-406-18

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 11
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-18

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 12
US-10-977-087-18
; Sequence 18, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; TITLE OF INVENTION: AND THEIR METHODS OF USE V
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-087-18

Query Match   100.0%; Score 1670; DB 5; Length 313;
Best Local Similarity   100.0%; Pred. No. 2.2e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
         |||||||||||||
Db  301 EIHLHSLSPGPSK 313
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RESULT 13
US-10-941-635-1

; Sequence 1, Application US10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-941-635-1

Query Match   100.0%;   Score 1670;   DB 5;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 2.2e-143;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 14
US-10-941-635-152

; Sequence 152, Application US10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 152
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence

US-10-941-635-152

Query Match   100.0%;   Score 1670;   DB 5;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 2.2e-143;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
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Db  301 EIHLHSLSPGPSK 313
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RESULT 15
US-10-620-052A-22

; Sequence 22, Application US10620052A
; Publication No. US20040126784A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasunichi
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Markovtsov, Vadim
; APPLICANT: Rigel Pharmaceuticals, Inc.

```
;  TITLE OF INVENTION: Modulators of Cellular Proliferation
;  FILE REFERENCE: 021044-0040100US
;  CURRENT APPLICATION NUMBER: US/10/620,052A
;  CURRENT FILING DATE:    2003-07-14
;  PRIOR APPLICATION NUMBER: US 60/395,443
;  PRIOR FILING DATE: 2002-07-12
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: Patentin Ver. 2.1
;
;  SEQ ID NO 22
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: PIM1 oncogene serine threonine kinase
US-10-620-052A-22

  Query Match      99.2%;     Score 1657;  DB 4;  Length 313;
  Best Local Similarity   99.4%;   Pred. No. 3.3e-142;
  Matches 311; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy      241 PFEHDEEIIRGQVFFRQRVSSECCOHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 PFEHDEEIIRGQVFFRQRVSSECCOHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy      301 EIHLHSLSPGPSK 313
            |||||||||||||
Db      301 EIHLHSLSPGPSK 313
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Search completed: May 4, 2006, 05:32:05
Job time : 94.6667 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbn** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbn** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:27:44 ; Search time 15.3333 Seconds
                 (without alignments)
                 944.812 Million cell updates/sec

Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL..........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues
Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA New:*
                 1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5: /SIDS5/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
                 6: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 7: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
                 9: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 10: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*
                 11: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep1:*
                 12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1128.5	67.6	455	9	US-10-784-004-373	Sequence 373, App
2	869.5	52.1	311	9	US-10-501-841-40	Sequence 40, Appli
3	869.5	52.1	311	11	US-10-501-841-40	Sequence 2, Appli
4	864	51.7	334	8	US-11-103-065-2	Sequence 2982, Ap
5	864	51.7	334	8	US-11-511-937-2982	Sequence 2982, Ap
6	384.5	23.0	256	9	US-10-501-841-32	Sequence 32, Appl
7	382.5	22.9	661	8	US-10-877-346-74	Sequence 74, Appl
8	376	22.5	950	8	US-10-505-928-690	Sequence 690, App
9	368.5	22.1	631	11	US-10-501-035-357	Sequence 357, App
10	366	21.9	504	11	US-11-241-056-11	Sequence 11, Appl
11	364.5	21.8	256	9	US-11-087-099-9816	Sequence 9816, Ap
12	364.5	21.8	256	11	US-10-877-346-72	Sequence 72, Appl
13	356	21.3	514	11	US-11-113-424-183	Sequence 183, App
14	352	21.1	512	11	US-11-087-099-11500	Sequence 11500, A
15	352	21.1	514	11	US-11-087-099-3997	Sequence 3997, Ap
16	348.5	20.9	619	11	US-11-087-099-12402	Sequence 12402, A
17	348.5	20.9	722	9	US-10-784-004-435	Sequence 435, App
18	348.5	20.9	722	9	US-10-784-004-951	Sequence 951, App
19	348	20.8	472	11	US-11-087-099-11838	Sequence 11838, A
20	346	20.7	86	9	US-10-501-841-37	Sequence 37, Appl
21	342.5	20.5	651	9	US-10-770-726-67	Sequence 67, Appl
22	342.5	20.5	651	11	US-11-177-138-10	Sequence 10, Appl
23	342	20.5	464	11	US-11-096-568A-22124	Sequence 22124, A
24	341	20.4	513	11	US-11-087-099-11726	Sequence 11726, A
25	340	20.4	620	11	US-11-087-099-3898	Sequence 3898, Ap
26	339.5	20.3	504	11	US-11-087-099-12331	Sequence 12331, A
27	339	20.3	713	9	US-10-995-561-881	Sequence 881, App
28	339	20.3	729	9	US-10-995-561-878	Sequence 878, App
29	339	20.3	744	9	US-10-995-561-880	Sequence 880, App
30	339	20.3	744	9	US-10-995-561-876	Sequence 876, App
31	339	20.3	753	9	US-10-995-561-877	Sequence 877, App
32	337.5	20.2	689	9	US-10-204-639-17	Sequence 17, Appl
33	336.5	20.1	445	11	US-11-096-568A-32575	Sequence 32575, A
34	336.5	20.1	448	11	US-11-096-568A-18364	Sequence 18364, A
35	333.5	20.0	1518	11	US-11-096-568A-18866	Sequence 18866, Ap
36	332	19.9	439	11	US-11-096-568A-20431	Sequence 20431, A
37	332	19.9	443	11	US-11-096-568A-20430	Sequence 20430, A
38	328.5	19.7	715	9	US-11-096-639-65	Sequence 65, Appli
39	327	19.6	582	11	US-11-979-095-6	Sequence 6, Appli
40	327	19.6	358	9	US-10-979-095-6	Sequence 4, Appli
41	327	19.6	765	11	US-11-096-568A-20431	Sequence 20431, A
42	326.5	19.6	765	11	US-11-096-568A-32895	Sequence 32895, A
43	325.5	19.5	278	8	US-10-370-959-17	Sequence 905, App
44	325.5	19.5	278	8	US-10-370-959-31	Sequence 31, Appl
45	325.5	19.5	278	9	US-10-055-877-149	Sequence 149, App

ALIGNMENTS

RESULT 1
US-10-784-004-373

; Sequence 373, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 373
; LENGTH: 455
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-373

Query Match   67.6%; Score 1128.5; DB 9; Length 455;
Best Local Similarity   72.2%; Pred. No. 2.5e-88;
Matches 213; Conservative 31; Mismatches 44; Indels 7; Gaps 5;

Qy   1 MLLSKINSLAHLRAAP-CNDLHATKLAPGK-EKEPLESQQYQVGPLLGSGDGFGSVYSGIR 57
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Db   130 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVVAGSR 188

Qy   58 VSDNLPVAIHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
              :|||||| || ||| |:|| || |||||||||||||| | ||||||||||||||||
Db   189 IADGLPVAVKHVVKERVIEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 247

Qy   116 FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILI 175
              |:|:|||||||||||||||||||||||||||||||||||||||||||||||||||:|:|:
Db   248 FLVLLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHCNCGVVHRDIKDENLLV 307

Qy   176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
              |:|||||||||||||||||||||||||||||||||||||||||:|:|||: |||||||||
Db   308 DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 367

Qy   236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
              ||||||||:|||||||| |||||||| |||:||||||||||||||||||||||||
Db   368 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERFSLDQIAAHPWM 422

RESULT 2

US-10-501-841-40
; Sequence 40, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
;   and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-01440PC2
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 40
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-40

Query Match   52.1%;   Score 869.5; DB 9;   Length 311;
Best Local Similarity   58.4%;   Pred. No. 1.7e-66;
Matches 167;   Conservative 39;   Mismatches 75;   Indels 5;   Gaps 2;

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Qy  28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
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Db  22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy  88 MEVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELAR 145
         | | ||||   | ||||||||||||| :| ||:|||| ||||| |||| ||  |
Db  82 LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy 146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTDFDGTR 205
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Qy 206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSSECQH 265
        |||||||  :| ||| ||:|||||||||||||||||||  ||:|:| ||  |  |: |
Db 202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQELEAELHFPAHVSPDCCA 261

Qy 266 LIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSPGP 311
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Db 262 LIRCLAPKPSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP 304
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RESULT 3
US-11-103-065-2
; Sequence 2, Application US/11103065
; Publication No. US20050282189A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E., Lora, Jose M.
; TITLE OF INVENTION: 2150, Human Protein Kinase Family
; FILE REFERENCE: MPI2001-137P1RNM
; CURRENT APPLICATION NUMBER: US/11/103,065
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: US/10/184,563
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,702
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-103-065-2

Query Match   52.1%;   Score 869.5; DB 11; Length 311;
Best Local Similarity   58.4%;   Pred. No. 1.7e-66;
Matches 167;   Conservative 39;   Mismatches 75;   Indels 5;   Gaps 2;

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Qy  28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
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Db  22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy  88 MEVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELAR 145
         | | ||||   | ||||||||||||| :| ||:|||| ||||| |||| ||  |
Db  82 LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy 146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTDFDGTR 205
        :|| || :| ||||| ||||||||||||||||||:|| ||||||||||||:|  ||||||
Db 142 CFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR 201

Qy 206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSSECQH 265
        |||||||  :| ||| ||:|||||||||||||||||||  ||:|:| ||  |  |: |
Db 202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQELEAELHFPAHVSPDCCA 261

Qy 266 LIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSPGP 311
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Db 262 LIRCLAPKPSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP 304
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RESULT 4
US-10-511-937-2982
; Sequence 2982, Application US/10511937
; Publication No. US20060088364A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;   AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 2982
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2982

Query Match   51.7%;   Score 864; DB 8;   Length 334;
Best Local Similarity   61.3%;   Pred. No. 5.5e-66;
Matches 163;   Conservative 37;   Mismatches 64;   Indels 2;   Gaps 1;

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Qy  28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
          |:||:|| :| |||||:|||||:|:|| :|||:|||:|||||:|||:| :||||||||
Db  22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy  88 MEVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELAR 145
         | | ||||   | ||||||||||||| :| ||:|||| ||||| |||| ||  |
Db  82 LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141
```

```
RESULT 5
US-10-501-841-32

; Sequence 32, Application US/10501841
; Publication No. US20060840055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058.01440ZPC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-32

Query Match     51.7%;  Score 864;  DB 9;  Length 334;
Best Local Similarity   61.3%;  Pred. No. 5.5e-66;
Matches 163;  Conservative 37;  Mismatches 64;  Indels 2;  Gaps 1;

Qy   28 GREKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
            | |:|:|::|| |||:||||| :| :||||:.|.||:|:..|::.|.:|. : :
Db   22 GKDREAFEAEYRLGPLLGKGGFGGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy   88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELAR 145
         :|| :|.|::  |||::||||||||:..:|.|.|.|:|||.:||||||||:..|:||||.
Db   82 LEVALLMKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy  146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTFDFDGTR 205
         .||.||:|| :||.|||||||||||||||||.||| ||||||||||||.|: ||.|||||
Db  142 CFFGQVVAAIQHCSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR 201

Qy  206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQRVSSECQH 265
         |||||||.|:|:|. ||:|||||||||||||||||||:.:|.:||||||||||.:.:.:
Db  202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261

Qy  266 LIRWCLALRPSDRPTFEEIQNHPWMQ 291
         ||| |||:||.|||:||||:|||||||
Db  262 LIRRCLAPKPSSRPSLEEILLDPWMQ 287


RESULT 6
US-10-877-346-74
; Sequence 74, Application US/10877346
```

```
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

Query Match     23.0%;  Score 384.5;  DB 9;  Length 256;
Best Local Similarity   37.0%;  Pred. No. 2.5e-25;
Matches 98;  Conservative 37;  Mismatches 98;  Indels 23;  Gaps 9;

Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
         :|:| ||||| ||.||.|. ||:.| :|||||. ::   |.:|.:::   :|:|:
Db    1 YELGEKLGSGAFGKVYKGKHKDIGEIVAIKILKRSLSE----KKKRFLREIQILRRLS 55

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR 156
          :.:.||.|.:::::.:::|::|||:| |||||:.::|: |:..|.|::
Db   56 --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRRNGLLSEKEAKKIALQILRGLE 112

Qy  157 HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVTVY--- 213
          .|:||:||||||.||||| |||:|.||||||::|||||||:|
Db  113 YLHSRGIVHRDLKPENILLDEN-GTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL 171

Qy  214 RYHRYHGRSAAVWSLGILLYDMVCGDIPF----EHDEEIIRGQVFFRQRV-----SSECQ 264
         .|:.|.|||.||.|.||:||||:|:||||    :||.|:.|.||:.:| .|..:
Db  172 EGRGYSSK-VDWWSLGVILYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK 230
```

RESULT 7

```
US-10-505-928-690
;  Sequence 690, Application US/10505928
;  Publication No. US20060088532A1
;  GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE: 2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
;  SEQ ID NO 690
;  LENGTH: 661
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-505-928-690

Query Match             22.9%;  Score 382.5;  DB 8;  Length 661;
Best Local Similarity   35.0%;  Pred. No. 1.2e-24;
Matches    93;  Conservative   49;  Mismatches  111;  Indels   13;  Gaps    8;

Qy         31 KEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEV 90
                |::  |:||  ||.|  |:|||.:|.||| :|:||..| |.:|:  ::
Db         48 KHNLKHRYELQETLGKGTYGKVKRATERFSGRVVAIKSIRKDKIKHDEQDM---VHIRRI 104

Qy         91 VLLKKVSSGFSGVIRLLDMFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQ 150
               :  ::  :||.||:  :   :..  |:|:|| : | .|::. : |:  | |:||:  :|
Db        105 EIMS--SLNHPHIISIYEVFENDKIVIIMEYASK-GELYDYISERRRLSERETRHFFRQ 161

Qy        151 VLEAVRHCHNCGVLHRDIKDENIILIDLNRGELKLIDFG-SGALLKDTVTDFDGTRVYSP 209
               ::.||::||: ||:||||| ||:|| | ||   || |:|  |.:| | :.|  ||||:|
Db        162 IVSAVHYCHKNGVVHRDLKLENILLDDN-CNIKIADFGLSNLYQKDKFLQTFCCSPLYAS 220

Qy        210 PEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFE-HDEEIIRGQVF---FRQRVS-SECQ 264
              ||:.      | ||.||:||:||: .:||  .|||   . :|| :|   |:||:|  :| |
Db        221 PEIVNGRPYRGPEVDSWALGVLLYTLVCGTMPFDGFDHKNLIRQISSGEYREPTQPSDAR 280

Qy        265 HLIRWCLALRPSDRPTFEEIQNHPWM 290
               .|||  |.:||  |:|  |:| ||:.
Db        281 GLIRWMLMVNPDRRATIEDIANHWVV 306
```

RESULT 8

```
US-10-501-035-357
;  Sequence 357, Application US/1050 1035
;  Publication No. US20060046249A1
;  GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING KINASE
;  TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE PATHWAYS
;  FILE REFERENCE: D0185 PCT
;  CURRENT APPLICATION NUMBER: US/10/501,035
;  CURRENT FILING DATE: 2004-07-09
;  PRIOR APPLICATION NUMBER: US 60/350,061
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 795
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 357
;  LENGTH: 950
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-501-035-357

Query Match             22.5%;  Score 376;  DB 9;  Length 950;
Best Local Similarity   32.4%;  Pred. No. 6.6e-24;
Matches    89;  Conservative   50;  Mismatches  114;  Indels   22;  Gaps    7;

Qy         38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
              |.: . ||.|..|.||. |.| :. . |||.:. :   .: |  .. | |:|::: ::  .
Db         44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL---DAVNLEKIYREVQIMKMLD 99

Qy         98 SGFSGVIRLLDMFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
               . | :: |: :.   :. :|::||.  | .:  :. .:  |   .: ||||::||.||.
Db        100 --HPHIIKIYQVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESEARKFWQILSAVDY 156

Qy        158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
              || :.|:|||:| ||:|:| ||   ||  || .| |:|  ::::||  |||  ||   .:
Db        157 CHGRKIVHRDLKAENLLLD-NNMMNIKIADFGFGNFFKSGGBLLATWCGSPPYAAPEVFEGQ 215

Qy        217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVSSECQHLIRWC 270
                .:  .:.:|:||::|:|: :|| :||         :|:   :   :||  :.|:||.
Db        216 QYEGPQLDIWSMGVVLYLVLVCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRM 275

Qy        271 LALRPSDRPTFEEIQNHPWM-------QDVLLPQE 298
              |.| |.:|:  |:|:  ||||      |  :|.||
Db        276 LVLDPSKRLTIAQIKEHKWMLIEVPVQQRVLYPQE 310
```

RESULT 9

```
US-11-241-056-11
;  Sequence 11, Application US/11241056
;  Publication No. US20060024807A1
;  GENERAL INFORMATION:
;  APPLICANT: Immunex Corporation
;  APPLICANT: Bird, Timothy A.
;  APPLICANT: Virca, G. Duke
;  APPLICANT: Martin, Unja
;  APPLICANT: Anderson, Dirk M.
;  TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
;  FILE REFERENCE: 2923-US
;  CURRENT APPLICATION NUMBER: US/11/241,056
;  CURRENT FILING DATE: 2005-09-30
;  PRIOR APPLICATION NUMBER: US/09/980,464
;  PRIOR FILING DATE: 2001-11-27
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 11
;  LENGTH: 631
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-11-241-056-11

Query Match             22.1%;  Score 368.5;  DB 11;  Length 631;
Best Local Similarity   33.4%;  Pred. No. 1.7e-23;
Matches    98;  Conservative   46;  Mismatches  116;  Indels   33;  Gaps    9;

Qy         22 ATKLAPGKEKEP-----------------LESQYQVGPLLGSGGFGSVYSGIRVSDNLPV 64
              |  ||.|.|:          :: .:. |  |||.|.||.|:.|||||:.    .|.|:|||
Db         24 ARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLLETLGKGTYGKVKA-RESSGRLV 82

Qy         65 AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDMFERPDSFVLILERPE 124
              |||.:  |:|.. | :    :.  |:|:::  .|.: ::| |  .. :.. |::::| |
Db         83 AIKSIRKDKIKHDEQDL---LHIRREIMS--SLNHPHIAIHEVFENSSKIVIMEYAS 137

Qy        125 PVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKL 184
              .| ||:|:|.||    ..|.|:| .|:|.||:|||: |:|||||| ||||:| ||   |
Db        138 R-GDLYDYISERPRLSERDARHFRQIVSALHYCHQNGIVHRDLKLENILDAN-GNIKI 195

Qy        185 IDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFE 243
              |||| :|.| |:  .:|  |  |:|||| :      |  ..||:|||:||: ::| |.|||
Db        196 ADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYRGPEVDSWSLGVLLYILLVHGTMPFD 255

Qy        244 HDE------EIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
              ||       :|||  . . :.||:. : .|||  |::|: || :.|:  ||:.
Db        256 GQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLEDVASHWWV 307
```

RESULT 10
US-11-087-099-9816
Publication No. US20060041961A1
GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11087099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match   21.9%; Score 366; DB 11; Length 504;
Best Local Similarity   34.4%; Pred. No. 2.1e-23;
Matches 90; Conservative 51; Mismatches 105; Indels 16; Gaps 8;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
         |:||  :||| ||||:|||:||:||:|| || || :|::| :| ::| |:||:|||:::
Db    8 YKLGKTLGISFGKVKIAEHALTGHKVAIKILNRRKIKN---LDMEEKVRREIKILRLFM   64

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQODLFDPITERGALQEELARSFFWQVLEAVRH 157
         |||  :||||| || ||:|| ||  ::|  :  | :|     |:||   || |: ||  :
Db   65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY  121

Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GIRVYSPPEWIRYH 216
         ||:|||||||||||||||:|||:||||||||||||| :|:| :|  |::||||||||||:
Db  122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IRGQVF-FRQRVSSECQHLIRW 269
         ||||||||||||||||| ||| |:| | |||       |||| |:|||||| |:| :|
Db  181 LYAGPEVDVVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy  270 CLAIRPSDRPTFEEIQNHPWMQ 291
         | | ||||||||||||||||||
Db  240 MLIVDPMKRITIPEIRQHPWFQ 261
```

RESULT 11
US-10-877-346-72
Sequence 72, Application US/10877346
Publication No. US20060141153A1
GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 2142-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27

; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/Threonine protein kinase Consensus
; OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match   21.8%; Score 364.5; DB 9; Length 256;
Best Local Similarity   33.3%; Pred. No. 1.2e-23;
Matches 89; Conservative 55; Mismatches 96; Indels 27; Gaps 8;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
         |:||  :|||:||:|| |||:|| || || :| :|  :| :::|||::|||:|||:::
Db    1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL---KKKKRERILREIKILKKLD   56

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQODLFDPITERGALQEELARSFFWQVLEAVRH 157
         |||  :||||| || ||:|||:|  |   ::| |     |:||   || |::||  :
Db   57 --HPNIVKLYDVFEDDDKLYLVMEYCEG-GDLFDLLKKRGRLSEDEARFYARQILSALEY  113

Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRY  215
         ||:|||||||:|:||:||:|||:|||||||||||| |  :|:|:|:|:||||||||||:
Db  114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy  216 HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFFRQ------------RVSSE 262
         :|||||||||||||||| ||| |:|:|  :| :|||||||           |||
Db  172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPKPPPPPPEWWISPE 228

Qy  263 CQHLIRWCLAIRPSDRPTFEEIQNHPW 289
         ||:||| || |||||||||||||||
Db  229 AKDLIKKLLVKDPEKRLTAEEALEHPF 255
```

RESULT 12
US-11-113-424-183
Sequence 183, Application US/11113424
Publication No. US20050260713A1
GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29

```
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 183
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-11-113-424-183

Query Match     33.3%;  Score 364.5;  DB 11;  Length 256;
Best Local Similarity   21.8%;
Matches    89;  Conservative    55;  Mismatches    96;  Indels    27;  Gaps    8;

Qy   38  YQVGPLLGSGGGFGSGVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
             ::|||
Db    1  YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKEKL------KKKKRERILREIKILKKLD   56

Qy   98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH   157
             :||||
Db   57  --HPNIVKLYDVFEDDDKLYIVMEYCEG--GDLFLLKKRGRLSEDEARFYARQLSALEY   113

Qy  158  CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY   215
             :|:||||
Db  114  LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL  171

Qy  216  HRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEIIRGQVFFRQ----------RVSSE  262
             :|
Db  172  GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPFPPPPEWKISPE  228

Qy  263  COHLIRWCLALRPSDRPTFEEIQNHPW  289
             :||
Db  229  AKDLIKLLVKDPEKRLTAEEALEHPF  255
```

```
RESULT 13
US-11-087-099-11500
; Sequence 11500, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11500
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-11-087-099-11500

Query Match     33.2%;  Score 356;  DB 11;  Length 514;
Best Local Similarity   21.3%;  Pred. No. 1.6e-22;
Matches    87;  Conservative    54;  Mismatches    105;  Indels    16;  Gaps    8;

Qy   38  YQVGPLLGSGGGFGSGVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
             :|:
Db   19  YKLGKTLGIGSFGKVKIAEHTLGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM   75

Qy   98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH   157
             :||||
Db   76  --HPHIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY  132
```

```
RESULT 14
US-11-087-099-3997
; Sequence 3997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3997
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-3997

Query Match     32.2%;  Score 352;  DB 11;  Length 512;
Best Local Similarity   21.1%;  Pred. No. 3.4e-22;
Matches    84;  Conservative    55;  Mismatches    108;  Indels    14;  Gaps    6;

Qy   38  YQVGPLLGSGGGFGSGVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
             :|:
Db   19  YKLGKTLGIGSFGKVKIAEHTLGHKVAVKILNRRKIRN---MDMEEKVSREIKILRLFM   75

Qy   98  SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH   157
             :||||
Db   76  HGH--ISRLYEVIETPSDIYVVMEYVKS--GELFDYIVEKGRLQEDEARNFFQQIISGVEY  132

Qy  158  CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY  216
             :|:||||
Db  133  CHINMVRRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  191

Qy  217  RYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECOHLIRWC  270
             :|||
Db  192  LYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIGKGGYITLPSHLSAGARDLIPRM  251

Qy  271  LALRPSDRPTFEEIQNHPWMQ  291
             :|
Db  252  LIVDPMKRMTIPEIRLHPWFQ  272
```

```
RESULT 15
US-11-087-099-3612
; Sequence 3612, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3612
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-3612

Query Match     21.1%;  Score 352;  DB 11;  Length 514;
```

```
Best Local Similarity  32.2%;   Pred. No. 3.4e-22;
Matches   84;  Conservative   55;  Mismatches  108;   Indels   14;   Gaps   6;

Qy     38 YQVGPLLGSSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
          |:||.|||||||:|:|:|:  |:.|  ||| |.  |||||| |.|:|||
Db     19 YRLGKTLGIGSFGKVKIAEHTLIGHKVAVKILNRKIRN---MDMEEKVSREIKILRLFM 75

Qy     98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
          :  :  :|:::|:.|||::||:|:|:|::|:  :
Db     76 HGH--ISRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132

Qy    158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
          ||  ||:||:||:||| :|:.:: || ||| |||.|.||:|:|||
Db    133 CHINMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191

Qy    217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC 270
          || | |.:|.|||||||:||| |||||    ::|| :::  :|:|:.|
Db    192 LYAGPEVDVWSCGVILYALLCGTLPFFDDENIPNLFKKIKGGYITLPSHLSAGARDLIPRM 251

Qy    271 LALRPSDRPTFEEIQNHPWMQ 291
          |:  ||||:|.||:||:|||
Db    252 LIVDPMKRMTIPEIRLHPWFQ 272
```

```
                    GenCore version 5.1.7
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:            May  4, 2006, 05:12:40 ; Search time 113.667 Seconds
                                            (without alignments)
                                            1209.902 Million cell updates/sec

Title:             US-10-705-757-2
Perfect score:     1670
Sequence:          1 MLLSKINSLAHLRAAPCNDL..........LLPQETAEIHLHSLSPGPSK 313

Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched:          243163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:    2443163

Minimum DB seq.length: 0
Maximum DB seq.length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         A_Geneseq_21:*
                   1: geneseqp190s:*
                   2: geneseqp1990s:*
                   3: geneseqp2000e:*
                   4: geneseqp2001s:*
                   5: geneseqp2002s:*
                   6: geneseqp2003as:*
                   7: geneseqp2003bs:*
                   8: geneseqp2004s:*
                   9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

Result                  %      Query
  No.   Score   Match Length  DB    ID          Description
------  -----   ----- ------  --    --          -----------
   1    1670    100.0   313    5    ABP54943    Abp54943 Human Pim
   2    1670    100.0   313    6    ABG33017    Abg33017 Human pro
   3    1670    100.0   313    6    AAO19788    Aao19788 Human PIM
   4    1670    100.0   313    7    ABU61613    Abu61613 Human PIM
   5    1670    100.0   313    7    ABR62939    Abr62939 Human ser
   6    1670    100.0   313    7    ADE55368    Ade55368 Human Pro
   7    1670    100.0   313    7    ADF45083    Adf45083 Human kin
   8    1670    100.0   313    8    ADO19690    Ado19690 Human PRO
   9    1670    100.0   313    8    ADR88370    Adr88370 Human PIM
  10    1670    100.0   313    8    ADP24227    Adp24227 PRO polyp
  11    1670    100.0   313    8    ADT07365    Adt07365 Human pro
  12    1670    100.0   313    9    ADT14636    Adt14636 human Pim
  13    1670    100.0   313    9    ADY86782    Ady86782 Human Pim
  14    1670    100.0   313    9    AEA89424    Aea89424 Human Pim
  15    1670    100.0   313    9    AEB96037    Aeb96037 Human PIM
  16    1670    100.0   313    2    AAW08139    Aaw08139 Human cyt
  17    1657    99.2    313    3    AAY87959    Aay87959 Human CR7
  18    1657    99.2    313    8    ADI57202    Adi57202 Human PIM
  19    1657    99.2    313    8    ADN03170    Adn03170 Human PIM
  20    1657    99.2    313    9    ADY85580    Ady85580 Catalytic
  21    1636    98.0    313    5    ABG33016    Abg33016 Rat prote
  22    1636    98.0    313    6    AAO19789    Aao19789 Rat PIM1
  23    1636    98.0    313    7    ABR62938    Abr62938 Rat serin
  24    1636    98.0    313    9    AEB96039    Aeb96039 Norway ra
  25    1582    94.7    313    5    ABG33015    Abg33015 Mouse pro
  26    1582    94.7    313    6    AAO19790    Aao19790 Murine PI
  27    1582    94.7    313    6    ABR62940    Abr62940 Mouse ser
  28    1582    94.7    313    7    ADN97347    Adn97347 Murine Pi
  29    1582    94.7    313    8    ADR88371    Adr88371 Mus muscu
  30    1582    94.7    313    9    AEA19261    Aea19261 Mouse Pim
  31    1582    94.7    313    9    AEB96041    Aeb96041 House mou
  32    1576    94.4    313    9    AEA19263    Aea19263 Mouse Pim
  33    1362    81.6    253    8    ADI57241    Adi57241 PIM1 domi
  34   1296.5   77.5    257    2    AAY43942    Aay43942 Rat prote
  35   1294.5   77.5    254    8    ADK71853    Adk71853 Human kin
  36    1255    75.1    233    8    ADT07367    Adt07367 Human pro
  37    1140    68.3    233    2    ADR88376    Adr88376 Columnix
  38    1135    68.0    323    8    AAY06886    Aay06886 HWHJ20 p
  39    1135    68.0    374    8    ADX91611    Adx91611 Plant ful
  40    1133    67.8    326    4    ADX91612    Adx91612 Plant ful
  41    1133    67.8    326    5    AAE23834    Aae23834 Human ser
  42    1133    67.8    326    5    ABG33011    Abg33011 Human HKI
  43    1133    67.8    326    7    ABR62932    Abr62932 Human ser
  44    1133    67.8    326    7    ADJ96625    Adj96625 Human pro
  45    1133    67.8    326    8    ADL97960    Adl97960 Human PIM
```

                                ALIGNMENTS

RESULT 1
ID   ABP54943
AC   ABP54943;
XX
DT   13-JAN-2003 (first entry)
XX
DE   Human Pim1.
XX
KW   Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW   mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW   human; gene therapy.
XX
OS   Homo sapiens.
XX
XX
FH
PN   WO20026444-A1.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005278.
XX
PR   21-FEB-2001; 2001US-0271254P.
XX
PA   (CHIR) CHIRON CORP.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2002-698650/75.
DR   N-PSDB; ABV73989.
XX
PT   Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT   Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT   abnormal expression levels and activity of TTK, such as lung, colon,
PT   prostate and ovarian cancer.
PS   Disclosure; Page 80-81; 113pp; English.
CC
CC   The present sequence is the protein sequence of human Pim1, a protein
CC   related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC   polynucleotides and polypeptides of the invention encompass
CC   polynucleotides and polypeptides having sequence similarity or sequence
CC   identity to human TTK and other genes and gene products related to TTK,
CC   such as Pim1. The invention is based on the finding that TTK is
CC   differentially expressed in various forms of cancer. It provides methods
CC   for the identification of cancerous cells, especially breast cancer and
CC   colon cancer cells, by detection of expression levels of TTK, as well as

CC   diagnostic, prognostic and therapeutic methods. These methods can be used
CC   as the basis of rational therapy. Assays for identifying molecules that
CC   modulate the activity of these genes in cancer, as well as methods of
CC   inhibiting tumour growth by inhibiting the activity of TTK are also
CC   provided
XX
SQ   Sequence 313 AA;

Qy   Query Match   100.0%; Score 1670; DB 5; Length 313;
     Best Local Similarity   100.0%; Pred. No. 1.4e-154;
     Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSGVSYSGIRVSD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSGVSYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
           |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 2
AC   ABG33017
ID   ABG33017 standard; protein; 313 AA.
XX
AC   ABG33017;
XX
DT   20-DEC-2002 (first entry)
XX
DE   Human protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; human.
XX
OS   Homo sapiens.
XX
PN   US20021151 20-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX

PS   Example 3; Page 40-41; 48pp; English.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cancer or haematopoietic neoplastic
CC   differentiative disorders including cancer or cellular proliferative and/or
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a human protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Qy   Query Match   100.0%; Score 1670; DB 5; Length 313;
     Best Local Similarity   100.0%; Pred. No. 1.4e-154;
     Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSGVSYSGIRVSD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSGVSYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
           |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 3
AC   AAO19788
ID   AAO19788 standard; protein; 313 AA.
XX
AC   AAO19788;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Homo sapiens.
XX
PN   WO20029317 3-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX

DR   WPI; 2003-120715/11.
DR   N-PSDB; AB269186.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 6; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
          |||||||||||||
Db  301 EIHLHSLSPGPSK 313
```

RESULT 4
ID   ABU61613 standard; protein; 313 AA.
XX
AC   ABU61613;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Human PIM1 protein.
XX
KW   Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW   mitotic checkpoint gene; PIM1.
OS   Homo sapiens.
XX
PN   US2003045491-A1.
XX
PD   06-MAR-2003.
XX
PF   21-FEB-2002; 2002US-00080119.
PR   23-FEB-2001; 2001US-0289813P.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A. B.
PA   (CHAN/) CHAN V W.

XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   WPI; 2003-456566/43.
DR   N-PSDB; ACA62265.
XX
PT   Detecting cancer in a subject, by comparing expression levels of tyrosine
PT   threonine kinase polypeptide or polynucleotide in a subject cell and a
PT   normal cell, where an increase in the expression level in the test cell
PT   is indicative of cancer.
XX
PS   Disclosure; Page 34-35; 79pp; English.
XX
CC   The invention relates to detecting cancer (other than ovarian cancer) in
CC   a subject, comprising comparing the expression levels of tyrosine
CC   threonine kinase (TTK), a mitotic checkpoint gene) polypeptide or
CC   polynucleotide in a test cell obtained from the subject and in a normal
CC   non-cancer cell, where an increase in the expression level of TTK protein
CC   or nucleic acid in the test cell compared to that in the normal cell
CC   indicates the presence of cancer other than ovarian cancer. Also included
CC   are reducing growth of a cancerous cell (by contacting a cancerous cell
CC   with an amount of an agent effective to reduce TTK polypeptide activity
CC   in the cell), an assay for identifying a candidate agent that reduces
CC   growth of a cancerous cell (comprising: (i) detecting the activity of a
CC   TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC   the activity of TTK polypeptide in the presence of a candidate agent
CC   relative to TTK polypeptide activity in the absence of the candidate
CC   agent), identifying an agent that reduces TTK activity (comprising: (i)
CC   contacting a cancerous cell displaying elevated expression of a TTK-
CC   encoding polynucleotide with a candidate agent; and (ii) determining the
CC   effect of the candidate agent on TTK polypeptide activity) and assessing
CC   the prognosis of a cancerous disease other than ovarian cancer in a
CC   subject (comprising: (i) detecting expression of TTK -encoding
CC   polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC   level of expression of TTK-encoding polynucleotide in the test cancer
CC   cell with a level of expression of the polynucleotide in a control non-
CC   cancer cell, where the level of expression of TTK in the test cancer cell
CC   relative to the level of expression in the control non-cancer cell is
CC   indicative of the prognosis of the cancerous disease). The methods are
CC   useful for detecting cancer (other than ovarian cancer) in a subject,
CC   reducing growth of a cancerous cell, identifying a candidate agent that
CC   reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC   activity and assessing the prognosis of a cancerous disease other than
CC   ovarian cancer. The methods are also useful for determining the ability
CC   of a subject to respond to a particular therapy e.g. as a basis of
CC   rational therapy. The present sequence represents a closely related
CC   protein to human TTK, in this case human PIM1 (not defined)
XX
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
```

```
Qy      301 EIHLHSLSPGPSK 313
            |||||||||||||
Db      301 EIHLHSLSPGPSK 313
```

RESULT 5
ID   ABR62939 standard; protein; 313 AA.
XX
AC   ABR62939;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Human serine/threonine protein kinase PIM-1.
XX
KW   Human; PIM-1; protein kinase; enzyme.
XX
OS   Homo sapiens.
XX
XX
PN   WO2003060130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-0001401.
XX
PA   (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 40; 40pp; English.
XX
CC   The present sequence is the protein sequence of the human
CC   serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC   are paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC   and ABR62933) of the invention, which are therefore expected to be
CC   involved in cancer and cell growth regulation. PIM-3 is also involved in
CC   the development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
SQ   Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
```

```
Qy      181 ELKLIDFGSSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 ELKLIDFGSSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy      241 PFEHDEEIIRGQVFFRQRVSSECQOHLIRWCLALRPSDRPTFEEIQNHPWMQDLVLLPQETA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 PFEHDEEIIRGQVFFRQRVSSECQOHLIRWCLALRPSDRPTFEEIQNHPWMQDLVLLPQETA 300

Qy      301 EIHLHSLSPGPSK 313
            |||||||||||||
Db      301 EIHLHSLSPGPSK 313
```

RESULT 6
ID   ADE55368 standard; protein; 313 AA.
XX
AC   ADE55368;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Human Protein AAA60089, SEQ ID NO 1183.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
XX
PN   WO200316475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAA60089.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide sequence or the
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
SQ Sequence 313 AA;
XX

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313
```

RESULT 7
ADF45083
ID ADF45083 standard; protein; 313 AA.
XX
AC ADF45083;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase PIM1.
XX
KW Human; protein kinase; enzyme; inhibitor; PIM1.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 52; 260pp; English.
XX

CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
CC
SQ Sequence 313 AA;
XX

Query Match   100.0%; Score 1670; DB 7; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313
```

RESULT 8
ADO19690
ID ADO19690 standard; protein; 313 AA.
XX
AC ADO19690;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #308.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX

PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-420067/39.
DR N-PSDB; AD019689.
XX
PR 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411399P.
PR 20-SEP-2002; 2002US-0412314P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PT Novel PRO polypeptide e.g. PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX
PS Claim 7; SEQ ID NO 616; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
               |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 9
AC ADR88370
ID ADR88370 standard; protein; 313 AA.
XX
AC ADR88370;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human PIM 1 protein.
XX
KW Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS Homo sapiens.
XX
PN US2004171062-A1.

XX
PD 02-SEP-2004.
XX
PD 28-FEB-2003; 2003US-00377268.
XX
PF 28-FEB-2002; 2002US-0360651P.
PR 16-SEP-2002; 2002US-0411399P.
PR 20-SEP-2002; 2002US-0412314P.
PR 02-JAN-2003; 2003US-0437929P.
XX
PI Hirth K, Milburn MV;
XX
DR WPI; 2004-642017/62.
XX
PT Designing a ligand binding to a target molecule, comprises identifying as
PT molecular scaffolds compounds binding to members of a molecular family,
PT detecting orientation of scaffolds at a binding site of target, and
PT synthesizing ligand.
XX
PA (PLEX-) PLEXXIKON INC.
XX
PS Disclosure; SEQ ID NO 9; 186pp; English.
XX
CC The present invention relates to a method of designing a ligand binding
CC to a target molecule. The method involves identifying as molecular
CC scaffolds compounds binding to members of a molecular family, detecting
CC orientation of scaffolds at a binding site of target, and synthesising
CC ligand. The invention is useful for designing drug products and for
CC designing ligand binding to target molecules such as nuclear hormone
CC receptors, TNF receptors, G-protein coupled receptors, methyl
CC transferases, ligases, etc. The present sequence is the human PIM 1
CC protein. This sequence is used to illustrate the method of invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
               |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 10
AC ADP24227
ID ADP24227 standard; protein; 313 AA.
XX
AC ADP24227;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:1405.

XX
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX
PN WO200041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR N-PSDB; ADP24226.
XX
PT Claim 7; SEQ ID NO 1405; 2940pp; English.
XX
PS Claim 7; SEQ ID NO 1405; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180

Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180

Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILIDLNRG 180
Qy   181 ELKIDFGSSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Db   181 ELKIDFGSSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
Qy   241 PFEHDEEIIRGQVFFRORVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Db   241 PFEHDEEIIRGQVFFRORVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Qy   301 EIHLHSLSPGPSK 313
Db   301 EIHLHSLSPGPSK 313

RESULT 11
ID ADT07365 standard; protein; 313 AA.
XX
AC ADT07365;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human protein #1 associated to anticancer compound screening method.
XX
PF 05-APR-2004; 2004WO-JP004917.
XX
PR 03-APR-2003; 2003US-0459644P.
XX
PA (ONCO-) ONCOREX INC.
XX
PI Kobayashi M, Jian C;
XX
DR WPI; 2004-748778/73.
DR N-PSDB; ADT07366.
XX
PT Disclosure; SEQ ID NO 1; 93pp; Japanese.
XX
OS Homo sapiens.
XX
KW Prophylactic-therapeutic agent; apoptosis inducing agent;
KW anticancer agent; serine/threonine kinase Pim-1; cancer; solid tumour;
KW human.
XX
CC The invention relates to a method of screening a prophylactic-therapeutic
CC agent for an apoptosis inducing agent or an enhancer of an anticancer
CC agent. The method involves the use of a serine/threonine kinase Pim-1,
CC its partial peptide or its salt. Also disclosed is a kit for carrying out
CC the method of the invention. The method is useful for screening a
CC prophylactic-therapeutic agent for cancer. The method is also useful for
CC prophylaxis and/or treatment of cancer, inducing apoptosis, treating a
CC patient having a solid tumour that is resistant to an anticancer agent
CC (induced by hypoxia), and for screening a substance that promotes or
CC inhibits the activity of serine/threonine kinase Pim-1. The present
CC sequence represents a human polypeptide relating to the present
CC invention.
XX
SQ Sequence 313 AA;

Query Match   100.0%; Score 1670; DB 8; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60

RESULT 12
ADT14636

```
ID   ADT14636 standard; protein; 313 AA.
XX
AC   ADT14636;
XX
DT   13-JAN-2005  (first entry)
XX
DE   human Pim-1 (oncogene-encoded serine/threonine kinase) protein.
XX
KW   crystallography; Pim-1; cancer; serine/threonine kinase; enzyme;
KW   protein co-ordinate data; protein structure.
XX
OS   Homo sapiens.
XX
PN   WO200409006-A2.
XX
PD   21-OCT-2004.
XX
PF   01-APR-2004; 2004WO-US010345.
XX
PR   04-APR-2003; 2003US-0460843P.
PR   12-MAR-2004; 2004US-0552526P.
XX
PA   (VERT-) VERTEX PHARM INC.
XX
PI   Jacobs ML, Hare B, Swenson L;
XX
DR   WPI; 2004-757977/74.
XX
FH   Key             Location/Qualifiers
FH
FT   Domain          33..121
FT                   /note = N-terminal domain
FT   Domain          44..52
FT                   /note = Glycine-rich loop
FT   Domain          122..127
FT                   /note = Hinge region
FT   Domain          128..305
FT                   /note = C-terminal domain
FT   Modified-site   166
FT                   /label= OTHER
FT                   /note= "OTHER = Forms a salt bridge via linkage to
FT                   Asp200"
FT   Modified-site   200
FT                   /label= OTHER
FT                   /note = Activation loop
FT   Domain          186..210
FT                   /label= OTHER
FT                   /note= "OTHER = Forms a salt bridge via linkage to
FT                   Arg166"
XX
PT   Crystal useful for developing Pim-1 (oncogene-encoded serine/threonine
PT   kinase) inhibitors, comprises human Pim-1 protein, Pim-1 homologue, human
PT   Pim-1 protein complex, or Pim-1 homologue complex.
XX
PS   Claim 8; SEQ ID NO 2; 219pp; English.
XX
CC   The invention relates to a novel crystal comprising a human Pim-1
CC   (oncogene-encoded serine/threonine kinase) protein, a Pim-1 homologue, a
CC   human Pim-1 protein complex or a Pim-1 homologue complex. Pim-1 is
CC   primarily expressed in haemopoietic and germ cell lines and this
CC   expression is tightly regulated and induced by cytokines, mitogens and
CC   hormones. Human Pim-1 is associated with multiple cellular functions,
CC   such as proliferation, differentiation, apoptosis and tumourigenesis. The
CC   crystal of the invention relates particularly to the residues involved in
CC   the active site and binding sites of Pim-1. Such information may be
CC   useful for developing Pim-1 inhibitors that are useful as therapeutic
CC   agents in the treatment of cancer. The current sequence is that of the
CC   human Pim-1 (oncogene-encoded serine/threonine kinase) protein of the
CC   invention.
XX
SQ   Sequence 313 AA;
```

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301 EIHLHSLSPGPSK  313
        |||||||||||||
Db  301 EIHLHSLSPGPSK  313
```

RESULT 13
ADY86782

```
ID   ADY86782 standard; protein; 313 AA.
XX
AC   ADY86782;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human Pim1 protein, SEQ ID NO: 18.
XX
KW   Prognosis; cancer; cytostatic; neoplasm; tyrosine threonine kinase; TTK;
KW   Pim1.
XX
OS   Homo sapiens.
XX
PN   US2005063974-A1.
XX
PD   24-MAR-2005.
XX
PF   27-SEP-2004; 2004US-00951477.
XX
SQ   Sequence 313 AA;
```

```
Query Match             100.0%;  Score 1670;  DB 8;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 1.4e-154;
Matches  313;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD  60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301 EIHLHSLSPGPSK  313
        |||||||||||||
Db  301 EIHLHSLSPGPSK  313
```

```
PR   21-FEB-2001; 2001US-0271254P.
PR   23-FEB-2001; 2001US-0289813P.
PR   21-FEB-2002; 2002US-00081119.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
PS   Disclosure; SEQ ID NO 18; 78pp; English.

The invention relates to a method for assessing the prognosis of a
cancerous disease other than ovarian cancer which involves detection and
comparison of expression of a tyrosine threonine kinase (TTK)-encoding
polynucleotide in a test cancer cell with a control non-cancer cell. The
method is useful to assess the prognosis of a cancerous disease other
than ovarian cancer. It is useful to identify cancerous disease and to
determine the ability of a subject to respond to a particular therapy
e.g. as the basis of rational therapy. The present sequence is the TTK
related human Pim1 protein.

XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;
Matches 313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
          |||||||||||||
Db    301 EIHLHSLSPGPSK 313

RESULT 14
AEA89424
ID   AEA89424 standard; protein; 313 AA.
XX
AC   AEA89424;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human Pim1 protein, SEQ ID NO: 18.
XX
KW   Drug screening; diagnosis; therapeutic; cancer; cytostatic; neoplasm;
KW   Pim1.
```

```
XX
OS   Homo sapiens.
XX
PN   US2005130926-A1.
XX
PD   16-JUN-2005.
XX
PF   28-OCT-2004; 2004US-00977087.
XX
PR   06-NOV-1998; 98US-01071122P.
PR   06-JAN-1999; 99US-01148856P.
PR   14-MAY-1999; 99US-01341122P.
PR   26-JUL-1999; 99US-0145612P.
PR   13-AUG-1999; 99US-0148936P.
PR   03-NOV-1999; 99US-0433360.
PR   12-MAY-2000; 2000US-00570593.
PR   25-JUL-2000; 2000US-00626301.
PR   21-FEB-2001; 2001US-0271254P.
PR   21-FEB-2002; 2002US-00081119.
PR   06-FEB-2002; 2002US-00360848.
PR   30-OCT-2003; 2003US-00598959.
PR   22-JAN-2004; 2004US-00763692.
XX
DR   WPI; 2005-457024/46.
DR   N-PSDB; AEA89423.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Reinhard C, Jefferson AB, Chan VW, Kaufmann J, Xin H, Kennedy GC;
PI   Harrowe G, Khoja H, Shyamala V;
XX
PS   Disclosure; SEQ ID NO 18; 206pp; English.

The invention relates to human HX2004-6 protein and a seven transmembrane
receptor protein referred as VSHK-1 useful for diagnosing or treating
cancer. The invention also relates to a method for reducing the growth of
a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor
ligand and to identify a substance which modulates its signal
transduction activity. The HX2004-6 DNA is useful to detect the presence
of HX2004-6 in a biological sample (e.g. ductal epithelial cells from
tissue chosen from pancreas, colon and breast). The invention is useful
for screening drugs for the treatment of cancer. The present sequence is
the human Pim1 protein. This sequence is differentially expressed in
cancer cells.

XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;
Matches 313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
RESULT 15
AEB96037

ID    AEB96037 standard; protein; 313 AA.
XX
AC    AEB96037;
XX
DT    20-OCT-2005  (first entry)
XX
DE    Human PIM-1 serine-threonine kinase protein.
XX
KW    micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW    PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS    Homo sapiens.
XX
PN    DE102004004894-A1.
XX
PD    18-AUG-2005.
XX
PF    30-JAN-2004; 2004DE-10004894.
XX
PR    30-JAN-2004; 2004DE-10004894.
XX
PA    (CHEF ) GRUENENTHAL GMBH.
XX
PI    Christoph T;
XX
PT    Identifying substances that regulate PIM kinases, useful for treatment
PT    and diagnosis of urinary incontinence and the urge to urinate, and
PT    similar use of PIM proteins or nucleic acids.
XX
PS    Claim 1; Fig 1B; 37pp; German.
XX
CC    The invention relates to a novel method for identifying substances that
CC    regulate urinary incontinence and the urge to urinate. The method
CC    comprises incubating a test compound with a cell and/or cell preparation
CC    that has synthesized a specific protein of the PIM (proviral integration
CC    site) kinase family and measuring either binding of the test compound to
CC    the PIM kinase, or a functional parameter that is altered by the binding.
CC    The method of the invention demonstrates uropathic and gene therapy
CC    applications and may be useful for treatment and diagnosis of urinary
CC    incontinence and the urge to urinate. The method is based upon regulating
CC    the activity or expression of PIM kinases that are involved in bladder
CC    control. The current sequence is that of the human PIM-1 serine-threonine
CC    kinase protein of the invention.
XX
DR    WPI; 2005-556609/57.
DR    N-PSDB; AEB96036.
DR    REFSEQ; NP_002639.
XX
SQ    Sequence 313 AA;

Query Match             100.0%;  Score 1670;  DB 9;  Length 313;
Best Local Similarity   100.0%;
Matches 313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD   60

Qy    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy   241  PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA  300

Qy   301  EIHLHSLSPGPSK  313
          |||||||||||||
Db   301  EIHLHSLSPGPSK  313

Search completed: May  4, 2006, 05:24:45
Job time : 118.667 secs
```

OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: May 4, 2006, 05:19:22 ; Search time 20.3333 Seconds
                (without alignments)
                1481.107 Million cell updates/sec

Title: US-10-705-757-2
Perfect score: 1670
Sequence: 1 MLLSKINSLAHLRAAPCNDL.........LLPQETAEIHLHSLSPGPSK 313

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	313	1	TVHUP1	protein kinase (EC
2	1636	98.0	313	1	S26298	protein kinase (EC
3	1582	94.7	313	1	TVMSP1	protein kinase (EC
4	881.5	52.8	370	1	S55333	protein kinase pim
5	617	36.9	363	2	T22255	hypothetical prote
6	486	29.1	409	2	T15435	hypothetical prote
7	486	29.1	481	2	I49072	protein kinase - m
8	380	23.1	1398	2	T13741	hypothetical prote
9	376	22.8	1101	2	S66730	hypothetical prote
10	367	22.5	1358	2	S33653	probable serine/th
11	367	22.0	1358	2	T1049	probable serine/th
12	366	21.9	504	2	S55244	p69Eg3 protein - A
13	361	21.6	651	2	JC7500	qik protein - chic
14	361	21.6	798	2	JC1446	serine/threonine-s
15	360	21.6	512	1	A56609	serine/threonine-s
16	359	21.5	512	1	T52653	serine/threonine-s
17	357	21.4	511	1	T07788	SNF-related kinase
18	352	21.1	472	1	B90100	probable serine/th
19	348	20.8	469	2	B84644	hypothetical protein k
20	347.5	20.8	887	2	T20941	hypothetical prote
21	347.5	20.8	726	2	T33998	hypothetical prote
22	345	20.7	726	2	T04862	probable serine/th
23	342.5	20.5	489	2	T42953	hypothetical prote
24	342.5	20.5	1558	2	JN0323	Ca2+/calmodulin-de
25	341.5	20.4	414	1	S6304	serine/threonine-s
26	341	20.4	513	1	T07415	probable serine/th
27	339.5	20.3	504	2	T02306	probable serine/th
28	337	20.2	502	2	S27906	probable protein k
29	337	20.2	713	2	S27566	probable serine/th
29	336.5	20.1	445	2	T50802	serine/threonine p
30	335	20.1	745	2	G01025	serine/threonine p
31	333.5	20.0	1518	2	S37928	probable purine nu
32	331.5	19.9	774	2	I48609	probable serine/th
33	331	19.8	435	2	E84707	probable protein k
34	330.5	19.8	339	2	S56719	serine/threonine-s
35	330.5	19.8	520	2	G86414	probable protein k
36	330.5	19.8	553	1	T02139	calcium-dependent
37	328	19.6	591	2	S54788	calcium-stimulated
38	327	19.6	582	2	B84721	calcium-d
39	326.5	19.6	746	2	S62365	SNF1-related prote
40	325.5	19.5	442	2	T48203	probable calcium-d
41	325	19.5	1246	2	G89287	protein H3E23.1 (
42	324.5	19.4	713	2	T37886	hypothetical prote
43	324	19.4	401	2	B90120	probable serine/th
44	323	19.3	461	2	T14822	SNF1-related prote
45	323	19.3	473	1	S59941	probable serine/th

ALIGNMENTS

RESULT 1
TVHUP1
protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; UNIPARC:UPI000000001060; GB:M27903; NID:g189958; PID
A;Molecule type: mRNA
A;Residues: 1-313 <MEE>
A;Cross-references: UNIPARC:UPI000000001060; GB:M24779; NID:g1066790; PIDN:AAA81553.1; P
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
Gene 54, 105-111, 1987
A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
A;Reference number: A24476; MUID:88217423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Residues: 1-14, 'RA', 17-313 <ZAK>
A;Cross-references: UNIPARC:UPI000014987C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PI
R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immuno
A;Reference number: I58412; MUID:88217305; PMID:3329709
A;Accession: I58412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-313 <DOM>
A;Cross-references: UNIPARC:UPI000000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PI
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: GDB:PIM1
A;Map position: 6p21.2-6p21.2
A;Cross-references: GDB:119495; OMIM:164960
C;Genetics:
A;Gene: GDB:PIM1
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncoge
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif

F;67/Active site: Lys #status predicted

```
Query Match        100.0%;  Score 1670;  DB 1;   Length 313;
Best Local Similarity  100.0%;  Pred. No. 1.9e-76;
Matches  313;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
         |||||||||||||
Db   301 EIHLHSLSPGPSK 313
```

RESULT 2
S26298
protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S26298
R;Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
R;Title: Characterization of the testes-specific pim-1 transcript in rat.
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Accession: S26298
A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI0000131AD6; EMBL:X63675; NID:g56902; PID
A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcrip
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Function:
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Note: in testis may be involved in signal transduction events of normal germ cell matu
C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase homology <KIN>
C;Superfamily: protein kinase homology
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

```
Query Match        98.0%;  Score 1636;  DB 1;   Length 313;
Best Local Similarity  97.1%;  Pred. No. 9.2e-75;
Matches  304;  Conservative    6;  Mismatches   3;  Indels    0;  Gaps    0;

Qy     1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA 300
         ||||||||:.||||||||||||||||||||:|||||||:||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
         |||||||||||||
Db   301 EIHLHSLSPGPSK 313
```

RESULT 3
TVMSP1
protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.; v
Cell 46, 603-611, 1986
R;Title: The primary structure of the putative oncogene pim-1 shows extensive homology w
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI0000294AF; GB:M13945; GB:M13946; NID:g20
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni
A;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase homology <KIN>
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

```
Query Match        94.7%;  Score 1582;  DB 1;   Length 313;
Best Local Similarity  93.9%;  Pred. No. 4.4e-72;
Matches  294;  Conservative   10;  Mismatches   9;  Indels    0;  Gaps    0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||:||||||||||||||||||||||||||||||||:|
Db   121 ERPEPVQDLFDFITERGALQEELARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||:||||||||||||||||||:|||:|||| : ||||:|||||.|| ||||:
Db   241 PFEHDEEIIKGQVFFRQRVSSECQHLIKWCLSLRPSFEEIRNHPWMGDLLPQAAS 300

Qy   301 EIHLHSLSPGPSK 313
         |||||||||| ||
Db   301 EIHLHSLSPGSSK 313
```

RESULT 4
S55333
protein kinase pim-2 (EC 2.7.1.-) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Aller
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1
A;Reference number:
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPROT:Q62070; UNIPARC:UPI00000028629; GB:L41495; NID:g765065; PIDN:
A;Note: 34K form
A;Gene: CESP:P45H7,4
A;Map position: 3
C;Genetics:
C;Comment: Pim-2 autophosphorylates at unknown sites.
A;Accession: A43093
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

A;Reference number:
A;Accession: A43093
A;Molecule type: mRNA
A;Residues: 'M', 27-370 <VA2>
A;Cross-references: UNIPARC:UPI000000278BE; GB:L41495; NID:g765065; PID:
A;Note: 37K form
A;Molecule type: mRNA
A;Residues: 'M', 61-370 <VA3>
A;Cross-references: UNIPARC:UPI000000278BF; GB:L41495; NID:g765065; PIDN:AAA98924.1; PID:
A;Note: 40K form
A;Cross-references: UNIPROT:Q62070; UNIPARC:UPI000000278BE; GB:L41495; NID:g765065; PIDN:
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M', 27-370 <VA2>
A;Accession: S55333; A43093; B43093

Query Match   52.8%;
Best Local Similarity   56.6%;   Pred. No. 2.7e-37;
Matches 171; Conservative 41; Mismatches 85; Indels 5; Gaps 2;

```
Qy    12 LRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGSGFGSVYSGIRVSDNLPVAIKHVEK 71
            |: ::  ||| | |||||| |||||||||||||||||||| |||||  :|
Db    65 LQGHPSPPVTPQPPGGKDRAAFEAEYRLGPLLGKGGFGGTVFAGHRVTDRRQVAIKVISR 124

Qy    72 DRISDWGELPNGTRVPMEVVLLKKV- -SSGFSGVIRLLDWFERRPDSFVLILERPEPVQDL 129
           |:| :||||||||||||:||||||    :|: ||:|||||||| | :|: :|||||||||
Db   125 NRVLGWSTVSDSVTCPLEVALLWKVGEGNGHPGVIRLLDWFETPEGFMLVLERRMPAQDL 184

Qy   130 FDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRGELKLIDFGS 189
            ||||||||||||||||||||||||||||||||||||||||||||| :||  :|||||||
Db   185 FDYITEKGPLGESCSRSFFTQVVAAVQHCHARGVVHRDIKDENLILDLCRGSIKLIDFGS 244

Qy   190 GALLKDTVYTDFDPGTRVVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEII 249
            |||| ||| |||||||||||||||  | |||| ||||||||||||||||||||| ||:
Db   245 GALLHDEPYTDFDGDTRVVSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPFERDQEIL 304

Qy   250 RGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETAEIHLHSLSP 309
            |: |||||||| ||||: ||||: ||||||| |||| |||  |:|||  |:|||  | |
Db   305 EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSP 361

Qy   310 GP 311
           ||
Db   362 TP 363
```

RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T22255
R;Percy, C.
submitted to the EMBL Data Library, June 1994

A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI000001755A4; EMBL:Z34800; PIDN:CAA84323.
A;Experimental source: clone F45H7
A;Gene: CESP:F45H7,4

Query Match   36.9%;
Best Local Similarity   45.3%;   Score 617; DB 2;   Length 363;
Matches 120; Conservative 49; Mismatches 90; Indels 6; Gaps 3;

```
Qy    35 ESQYQVGPLLGSGSGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK 94
           |:::  |||  | ||||||||||||||  |||||||| | || ||||||||||||: |
Db    28 KKNYKLKAELGRGGFGVVTVRAVRICDNALVAVKFIERSNVKEWARI-NGEQVPMEICMLA 86

Qy    95 KVSSGFSGVIRLLDWFERRPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEA 154
           | :||| ||  ||||||  :  | : :|  |||||||||||||||||||||||||||||||
Db    87 KCSK-VRGVIRLLDWYSIPEGFLIVMERYPCIDMFDFIKGQGKISEDMARFLRQIAVT 145

Qy   155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDPGTRVVSPPEWIR 214
           ||:|  ||| |||||||:|:|| | ||| |||||||||||||||||||||||| ||||||
Db   146 VHECVQNRVLHRDLKDENIVIDLVTGSTKLIIDFGAATVLRRSQYSDFQGTRLYCPPEWFL 205

Qy   215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----IRGQVFFRQRVSSECQHLIRWC 270
           | : | |||||||||||||||||| |||| :|::    ||||||||||||| ||||:|
Db   206 HSLYLGREAAVWSLGVLLYNSLANGRLPFRNEKDICTAHLLGPLPFFVPVPVSAEVKDLISKC 265

Qy   271 LALRPSDRPTFEEIQNHPWMQDVLL 295
           ||| |||||||||| ||||||||||
Db   266 LTFDPFQRCSLEAILNHPWVKQQTL 290
```

RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid C06E8.
A;Reference number: Z18350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI000017B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN
A;Experimental source: strain Bristol N2
A;Gene: CESP:C06E8.3
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

Query Match   29.1%;
Best Local Similarity   35.8%;   Score 486; DB 2;   Length 409;
Matches 105; Conservative 55; Mismatches 125; Indels 8; Gaps 5;

```
Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGSGFGSVYSG-IRVS 59
           |:  | | |  | | ||:||||||||  |||||||||| ||||||||||||
Db     1 MIRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGGFIVYEATTRQD 56

Qy    60 DNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI 119
           :|||| || :|: | | |   |: || |  :  |::||| |  || :||||:||| | :
Db    57 GQQPVAVKFVQHKHVRSW-TMTCRQLFPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV 114

Qy   120 LERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN 178
           ||| |||||||| ||||||||||||||||||||||||||| |||||||||||||||| :
Db   115 MERPANCMDLFDWVSVHGPLNEDMGKFIFKQVITTVFNMYSKHGLLHRDIKDENLIVNMN 174
```

```
Qy    179  RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
               ||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||
Db    175  TGEVKLVDFGATAYAEKATKKEFQGTRSYCPPEWFRDQLYLPLEATSWSLGVLLFILLTG 234

Qy    239  DIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
               ||||  |:|    ::||||||||||||||||||||||||||||||||||||
Db    235  KLPFRNEIQICLGNVKFPPDLSKEVCQLVKSCLTTSARASLAQIAAHPWME 287
```

RESULT 7
I49072

protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
A;Reference number: I49071; MUID:95200798; PMID:7893599
A;Accession: I49072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

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Query Match             23.1%;  Score 386; DB 2;   Length 481;
Best Local Similarity   33.9%;  Pred. No. 1.3e-12;
  Matches  99;  Conservative  53;  Mismatches 120;  Indels  20;  Gaps  10;

Qy     18  NDLHATKLAPGKEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRIS 75
               :|| ::| |    : |: |  ||||||||| ||||| |||||||||||| ::|||||: |
Db     52  SEFRAVPSGTGRSQKPLRVGFYDVERTLGKGNFAVVKLRGHRVT-KTQVAIKIIDKTRL- 109

Qy     76  DWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITE 135
               | :|||||  ||| :||| : ||:|| ||||||||::|| :|| | |   : |:|:|:|
Db    110  --DSSNLEKIYREVQLMKLLN--HPNIIKLYQVMETKDMLYIVTEFAKN-GEMFDVLTS 163

Qy    136  RGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKIDENILIDLNRGELKLIDFGSGALLK- 194
               |||  |  || ||||||| |||||:|||||||:|||||||:||||||||||||||| |||
Db    164  NGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLDSNM-DIKLADFGFGNFYKP 222

Qy    195  DTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEI 248
               | ||||||||||:|||||||||||||||||||||||||||:|| ||||||     |||
Db    223  GEPLSTCVGSPPYVAAPEVEFGKEYEGPQLDVWSLGVVLVLVCGSLPFDGPNLPTLRQRV 282

Qy    249  IRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQ--DVLLPQE 298
               ||||||||||||||:||||||||||||||||||||||||||||  :||| |
Db    283  LEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQADPTLLQQD 334
```

```
Best Local Similarity   33.3%;  Pred. No. 6.2e-12;
  Matches  92;  Conservative  57;  Mismatches 109;  Indels  18;  Gaps   9;

Qy     29  KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRV 86
               :| |:: |  |||||||| ||||| |||||||||||||||||||| ::||:|:| |:||
Db    131  KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQ------DQTNLQKV 185

Qy     87  PMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARS 146
               |||| :||| :||:||||||||||||||||||| ||| ||||||||:|||||||||| ||
Db    186  YREVEIMKRLK--HPHIIKLYQVMETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy    147  FFWQVLEAVRHCHNCGVLHRDIKIDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
               |||||| ||||||:|||||||:|||||||:||||||||||||| ||| | | |||||||||
Db    243  KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP 301

Qy    206  VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIRGQVFFRQRV 259
               |:|||||||||||||||||||||||||||:|| ||||||      |||||||||||||||
Db    302  PYAAPEVFEGKQYTGPEIDIWSLGVVLYVLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM 361

Qy    260  SSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLL 295
               |||||||||||||||||||||||||||||||| :||
Db    362  SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397
```

RESULT 9
S66730

hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI000012DF35; EMBL:Z74788; NID:g1419846; PI
A;Experimental source: strain S288C
C;Genetics:
A;Map position: 15L
C;Keywords: ATP
F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

```
Query Match             22.5%;  Score 376; DB 2;   Length 1101;
Best Local Similarity   32.6%;  Pred. No. 8e-12;
  Matches  87;  Conservative  59;  Mismatches 105;  Indels  16;  Gaps   6;

Qy     36  SQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLL 93
               |:|:|||||||||||||||||||||||||||||||:|||  ::||:|||| ||||| ::|
Db    839  SDFTILQVWGEGAYGKVNLCIHRREHYIVVIKMLFKERLLVDVDTWVRDRKLGTIPSEIQM 898

Qy     94  KKVS-SGFSGVIRLLDWFERPDSFVLILERPEPVQ-----DLFDFITERGALQEELARS 146
               |||: ::|:||||||||||||||||||| |   ||     |||||:|||| |  |||| |
Db    899  ATLNKNSQENILKLLDFEDDYYI----ETPVHGETGSIDLFDVIEFKKDMVEHEAKL 954

Qy    147  FFWQVLEAVRHCHNCGVLHRDIKIDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRV 206
               |||||| |||||||:|||||||:||||||:||||||:||||||||||||||||||||||||
Db    955  VFKQVVASIKHLHDQGIVHRDIKHRDIKDENIVD-SHGFVKLIDFGSGAAYIKSGPFDVFVGTMD 1013

Qy    207  YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIRGQVFF--RQRVSSECQ 264
               ||||||||||||||||||||||||||||:|| ||||||::|||||||||  ||||||||
Db   1014  YAAPEVLGSSSYKGKPQDIWALGVLLYTIIYKENPYYNDEILEGELRFDKSEHVSECI 1073

Qy    265  HLIRWCLALRPSDRPTFEEIQNHPWMQ 291
               ||||||||||||||||||||||||||
Db   1074  SLIKRILTREVDKRPTIDEIYEDKWLK 1100
```

RESULT 8
T13741

hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217668
A;Accession: T13741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI000008201A3; EMBL:AL031765; NID:e1371523;
C;Genetics:
A;Cross-references: FlyBase:FBgn0000667
A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A;Note: EG:22E5.8

RESULT 10

S33653

probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
A;Reference number: S33653
A;Accession: S33653
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
A;Reference number: S36711
A;Accession: S36717
A;Molecule type: DNA
A;Residues: 1-864,867-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Fortin, N.; D
Yeast 8, 133-145, 1992
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptiona
A;Reference number: S36732
A;Accession: S36732
A;Cross-references: UNIPARC:UPI000017A44A; EMBL:S93805
R;Sidhu, R.S.; Mathews, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharomy
A;Reference number: JH0486
A;Accession: JH0486
A;Molecule type: DNA
A;Residues: 1-72, 'E', 74-154 <SID>
A;Cross-references: JH0483; MUID:92077420; PMID:1743509
C;Genetics:
A;Gene: SGD:FUN31; SSP138
C;Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
F;1096-1356/Domain: protein kinase homology <KIN>
F;1104-1112/Region: protein kinase ATP-binding motif
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1233/Active site: Asp #status predicted

Query Match   22.0%;   Score 367;   DB 2;   Length 1358;
Best Local Similarity   33.7%;   Pred. No. 2.7e-11;
Matches   87;   Conservative   53;   Mismatches 102;   Indels 16;   Gaps   6;

Qy   44 LGSGGFGSVYSGIRVSDNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF 100
                 ::|||||::||::||:|||||||:||||||: : ||:|||||||||||||||| :||
Db   1104 MGEGAYGKVNLCIHKKRYIVIVIKMIFKERILVDTWTWRDRKLGTIPSEIQIMATLNKKPH 1163

Qy   101 SGVIRLLDWFERPDSFVLILERPEPVQ-------DLFDFITERGALQEELARSFFWQVLEA 154
                 ::||||||||:||::||||||::||| ::|::|||||||||||::|:||::|
Db   1164 ENILRLLDFPFEDDDYVYI----ETPVHGETGCIDLFDLIEFKINMTEFEAKLIFKQVVAG 1219

Qy   155 VRHCHNCGVLHRDIKDENILILDLNRGELKLIDFGSGALLKDTVYTDFDGTRVSPPEWIR 214
                 |:||||:|||||||||||||:|:|:||||||||||||| ||||||||||||:|||||||:
Db   1220 IKHLHDQIVHRDIKDENIVLD-SKGFVKIIDFGSAAVKSGPFDVFVGTIDVYAAPEVLG 1278

Qy   215 YHRYHGRSAAVWSLGILLLYYDMVCGDIPEHDEEIIRGQVFFR--QRVSSECQHLIRWCLA 272
                 ||||||||||||||||||:||:||:||||||||: |:|||:|| :|:||:||:|||||
Db   1279 GNPYEGQPQDIWAIGILLYTVFVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN 1338

Qy   273 LRPSDRPTFEEIQNHPWM 290
                 ||| :|:| ||| |:
Db   1339 RCVPKRPTIDDINNDKWL 1356

RESULT 11

T10449

probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Accession: Z17020
A;Reference number: Z17020
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match   21.9%;   Score 366;   DB 2;   Length 504;
Best Local Similarity   34.4%;   Pred. No. 1.3e-11;
Matches   90;   Conservative   51;   Mismatches 105;   Indels 16;   Gaps   8;

Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
                 |:||:| |||:|||:||::||:|||||||:||||:||: ||:|||||||||||||||||
Db   8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN--LDMEEKVRREIKILRLFM 64

Qy   98 SGFGSVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
                 :|| |::||||||:||::||||||::||| :|:|||||||||||||::||||::|::|
Db   65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFQIISGVEY 121

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVSPPEWIRYH 216
                 ||:|||||||||||||:||:|:||||||||||||| ||||||||| |||||||||||||
Db   122 CHRMVVHRDLKPENLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy   217 RYHGRSAAVWSLGILLLYYDMVCGDIPEHDEEI------IRGQVF-FRQRVSSECQHLIRW 269
                 :||||||||||||||::||:||:|||||||::| :|:||| |:|:||:|||:|||
Db   181 LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELPS 239

Qy   270 CLALRPSDRPTFEEIQNHPWMQ 291
                 | || |||:||:||||||| |
Db   240 MLVVDPMKRITIPEIRQHPWFQ 261

RESULT 12

S52244

p69Eg3 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S52244
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Reference number: S52244
A;Accession: S52244
A;Description: Eg3, selected by differential screening encodes a new Xenopus protein k
A;Status: preliminary
A;Accession: S52243
A;Molecule type: mRNA
A;Residues: 1-651 <ROG>
A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; P
C;Keywords: ATP
F;11-265/Domain: protein kinase homology <KIN>
F;19-27/Region: protein kinase ATP-binding motif

Query Match   21.6%;   Score 361;   DB 2;   Length 651;
Best Local Similarity   34.8%;   Pred. No. 2.8e-11;
Matches   94;   Conservative   51;   Mismatches 103;   Indels 22;   Gaps   8;

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Qy   32 EPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
        :|::|  | |:||:||:|||::| |  :|:: : :||| :||
Db    7 EELLKYELHETVGTGGFAKVKLASHLITGEKVAIKIMDKESLGD--DLP---RVKTEID 61

Qy   92 LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARSFFWQV 151
        :  :  | | |   | : | |  .|::||| | :|||||:| :| |::|||||  |::|
Db   62 AMKNLS--HQHVCRLYHVIETPKKIFMVLEYC-PGGELFDYIIAKDRLTEEEARVFFRQI 118

Qy  152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-----GTRV 206
        : |  : |  | :|||:| |||:|:::  :|||||||  |   .  |            |
Db  119 VSAVAYIHSQGYAHRDLKPENLLIDEDQ-NLKLIDFGLCAKPKGGL--DYHLMTCCGSPA 175

Qy  207 YSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIIRGQVFFRQRVS 260
        |: ||      :| | |:| |||:| | ::||::|||:       : ::| |  :  :
Db  176 YAAPELIQGKAYIGSEADIWSMGVLMYALMCGYLPFDDDNVMVLYKKIMRGKYEIPKWLS 235

Qy  261 SECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
         . | ::    :  .  .|   ::  ||||
Db  236 PGSVLLLSQMMQVDPKKRITVKHLLNHPWL 265
```

RESULT 13
JC7500

qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
A;Molecule type: DNA
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: UNIPROT:Q91A88; UNIPARC:UPI000004792; GB:AF219232
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
C;Genetics:
A;Gene: qik
C;Keywords: protein kinase

Query Match   21.6%; Score 361; DB 2; Length 798;
Best Local Similarity   32.7%;
Matches   88; Conservative   50; Mismatches 115; Indels   16; Gaps 7;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db   26 YDIERTLGKGNFAVVKLARHRVTKTQVAIKIIDKTRL----DPSNLEKIYREVQIMKLLN 81

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db   82 --HPHIIKLYQVMETKDMLYIVTEFAKN-GEMFDHLTSNGHLSSSEARKRFWQLSAVEY 138

Qy  158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD-TVYTDFDGTRVYSPEWIRYH 216
Db  139 CHSHHIVHRDLKTENLLLDDANM-NIKLADFGFGNFYKSGGEPLSTWCGSPPYAAPEVFEGK 197

Qy  217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIIRGQVFFRQRVSSECQHLIRWC 270
Db  198 EYEGPHLDIWSLGVVLYVLCGSLPFDGENLPTLRQRVLEGRFRIPYFMSEDCETLIRRM 257

Qy  271 LALRPSDRPTFEEIQNHPWMQ-DVLLPQE 298
Db  258 LVVDPTKRITISQIKQHKWMQADPSLRQQ 286
```

RESULT 14
JC1446

serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004

C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; GB:M93023; NID:g166599; PIDN:
R;Thuemler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A;Reference number: S58266
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: UNIPARC:UPI00000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI
R;Thuemler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes 1
A;Reference number: S66334; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI00000009DEE0; EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PI
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Genetics:
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
A;Superfamily: protein kinase homology <KIN>
F:17-271/Domain: protein kinase homology motif
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match   21.6%; Score 360; DB 1; Length 512;
Best Local Similarity   33.6%;
Matches   90; Conservative   51; Mismatches 111; Indels   16; Gaps 8;

```
Qy   32 EPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db   13 ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAIKILNRRKIKN---MEMEBKVRREIK 69

Qy   92 LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARSFFWQV 151
Db   70 ILRLFM--HPHIIRLYEVIETPTDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126

Qy  152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-----GTRVYSPP 210
Db  127 ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185

Qy  211 EWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------IRGQVP-FRQRVSSEC 263
Db  186 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA 244

Qy  264 QHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
Db  245 RDLIPRMLVVDPMKRVTIPEIRQHPWFQ 272
```

RESULT 15
A56009

serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 05-Oct-2004
C;Accession: A56009
R;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cer

```
tase of Saccharomyces cerevisiae.
A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602; NID:g496384; PIDN:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match          21.5%;  Score 359;  DB 1;  Length 511;
Best Local Similarity  31.7%;  Pred. No. 2.9e-11;
Matches 86;  Conservative 54;  Mismatches 117;  Indels 14;  Gaps 6;

Qy     28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSDNLPVAIKHVEKDRISDWGELPNGTRVP 87
             |::|   |  | :|.|   | ||::|    | :|| ||   :   | |:  ::   :|
Db      9 GSSVESFLRNYKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIKN---MEMEEKVR 65

Qy     88 MEVVLLKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSF 147
             |:|||| |  | :   | || |  |: | || | | | ||  | |: | |  |:||
Db     66 REIKILRLFM--HPHIIRLYEVETPSDIYVVMEYVKS-GELFDYIIVEKGRLQEDEARKF 122

Qy    148 FWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRV 206
             |   | |::|    |:|||||:|||:| |: ::   ||||| ||  ||  ::| |:|
Db    123 FQQIISGVEYCHRNMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPN 181

Qy    207 YSPPEWIRYHRYHGRSAAVWSLGLILLYDMVCGDIPFEHD-----EEIIRGQVFFRQRVS 260
             |:| |  | | || | ::| |:|:|| |  |||||: |     : : | ||  ||
Db    182 YAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGMISLPSHLS 241

Qy    261 SECQHLIRWCLALRPSDRPTFEEIQNHPWMQ 291
             :| :|||| | |:|||||||||| ||  |:|
Db    242 AGARDLIPRMLIVDPMKRMTIPEIRMHPWFQ 272
```

Search completed: May 4, 2006, 05:25:50
Job time : 22.3333 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: May 4, 2006, 05:12:40 ; Search time 122 seconds
(without alignments)
1810.085 Million cell updates/sec

```
Title:                 1670
Perfect score:         1670
Sequence:    1 MLLSKINSLAHLRAAPCNDL..........LLPQETAEIHLHSLSPGPSK 313

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:    2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
             1: uniprot_sprot:*
             2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1670	100.0	313	2	PIM1_HUMAN	P11309	homo sapien
2	1670	100.0	313	2	PIM1_HUMAN	P11309	homo sapien
3	1659	99.3	313	1	Q57TH7_HUMAN	Q57h7	homo sapien
4	1656	99.0	313	1	PIM1_FELCA	Q95I0	felis silve
5	1636	98.0	313	1	PIM1_BOVIN	Q9n0p9	bos taurus
6	1587	95.0	313	2	PIM1_RAT	P26794	rattus norv
7	1582	94.7	313	2	Q8CFN8_MOUSE	Q8cfn8	mus musculu
8	1140	68.3	323	1	PIM1_MOUSE	P06803	mus musculu
9	1133	67.8	326	2	Q8QU85_COTJA	Q8qu85	coturnix co
10	1129.5	67.6	326	1	PIM3_HUMAN	Q86V86	homo sapien
11	1128.5	67.6	326	1	PIM3_MOUSE	P58750	mus musculu
12	1128.5	67.6	380	2	PIM3_RAT	O70444	rattus norv
13	1116	66.8	325	2	Q4V8M2_RAT	Q4v8m2	rattus norv
14	1105	66.2	323	1	Q811X8_MOUSE	Q811x8	mus musculu
15	1101	65.9	318	1	PIM3_XENLA	Q91822	xenopus lae
16	1092	65.4	337	2	Q6III_XENTR	Q6iii	xenopus tro
17	1065	63.8	316	2	Q5U489_XENLA	Q5u489	xenopus lae
18	881.5	52.8	311	2	Q4STF0_TETNG	Q4stf0	tetraodon n
19	881.5	52.8	370	1	Q8R2P0_MOUSE	Q8r2p0	mus musculu
20	869.5	52.1	311	1	PIM2_MOUSE	Q62070	mus musculu
21	854	51.1	311	2	PIM2_HUMAN	Q9p1w9	homo sapien
22	851	51.0	310	1	Q72VJ5_BRARE	Q72vj5	brachydanio
23	846	50.7	310	1	Q8JFW9_BRARE	Q8jfw9	brachydanio
24	844	50.5	310	2	PIM1_BRARE		brachydanio
25	799.5	47.9	310	2	Q6D152_BRARE	Q6d152	brachydanio
26	716.5	42.9	288	2	Q4TDC2_TETNG	Q4tdc2	tetraodon n
27	626	37.5	221	2	Q8R1Z0_MOUSE	Q8r1z0	mus musculu
28	617	36.9	500	2	Q61B7_CAEBR	Q61jb7	caenorhabdi
29	497	29.8	441	2	Q20443_CAEEL	Q20443	caenorhabdi
30	486	29.1	566	2	Q61ZZ8_CAEBR	Q61zz8	caenorhabdi
31	486	29.1	378	2	Q8T3F1_CAEEL	Q8t3f1	caenorhabdi
32	440	26.3	270	2	Q5SPE4_BRARE	Q5spe4	brachydanio
33	423	25.3	465	2	Q5SPF6_BRARE	Q5spf6	brachydanio
34	421.5	25.2	134	2	Q6P2J9_HUMAN	Q6p2j9	homo sapien
35	421	25.2	416	2	Q4RFY6_TETNG	Q4rfy6	tetraodon n
36	412	24.7	281	2	Q5SV44_BRARE	Q5sv44	brachydanio
37	403	24.1	125	2	Q6Q2K5_CANFA	Q6q2k5	canis famil
38	394.5	23.6	268	2	Q5PP9_BRARE	Q5pp9	brachydanio
39	391.5	23.4	578	2	Q5RH93_BRARE	Q5rh93	brachydanio
40	389.5	23.3	1383	1	PASK_MOUSE	PASK_MOUSE	mus musculu
41	388	23.2	463	2	Q5RG24_BRARE	Q5rg24	brachydanio
42	388	23.2	465	2	Q5RG26_BRARE	Q5rg26	brachydanio
43	388	23.2	465	2	Q8CEE6_MOUSE	Q8cee6	mus musculu
44	388	23.2	1385	2	Q5TYR9_BRARE	Q5tyr9	brachydanio
45	387	23.2	1107	2	Q6C310_YARLI	Q6c310	yarrowia li

ALIGNMENTS

RESULT 1
PIM1_HUMAN

```
PIM1_HUMAN       STANDARD;       PRT;   313 AA.
ID   PIM1_HUMAN
AC   P11309; Q96RG3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA   Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT   "Primary structure of the putative human oncogene, pim-1.";
RL   Gene 90:303-307(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA   Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT   "The cDNA sequence and gene analysis of the human pim oncogene.";
RL   Gene 54:105-111(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88217305; PubMed=3329709;
RA   Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA   Berns A.;
RT   "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT   and immunological identification of the in vitro synthesized PIM-1
RT   protein.";
RL   Oncogene Res. 1:103-112(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88115604; PubMed=3429489;
RA   Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT   "Cloning and characterization of the human PIM-1 gene: a putative
RT   oncogene related to the protein kinases.";
RL   J. Cell. Biochem. 35:105-112(1987).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length human
RL   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RL   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RL   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=2030009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RL   "Identification of heterochromatin protein 1 (HP1) as a
RL   phosphorylation target of the human pim-1 kinase and the effect of
RL   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [8]
RP   CHARACTERIZATION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RL   "Identification of the human pim-1 gene product as a 33-kilodalton
RL   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [9]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RL   Anticancer Res. 23:167-178(2003).
RA   Johnson T., Lilly M.B., Kraft A.S.;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RX   MEDLINE=22257470; PubMed=12680209;
RP   ------
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC   cells. May affect the structure or silencing of chromatin by
CC   phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC   hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC   WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html".
CC   ------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ------

DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; mRNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAA81553.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU03327; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWS; X-ray; A=1-313.
DR   PDB; 1YHS; X-ray; A=33-305.
DR   PDB; 1YI3; X-ray; A=33-305.
DR   PDB; 1YI4; X-ray; A=33-305.
DR   PDB; 2BIK; X-ray; A=33-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   PDB; 2BZH; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
FT   CONFLICT   15   16   RA -> RG (in Ref. 2).
FT   CONFLICT   67   67   AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA; 35686 MW; 35BA76D3668B69A3 CRC64;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
              |||||||||||||
Db   301 EIHLHSLSPGPSK 313

Query Match   100.0%; Score 1670; DB 1; Length 313;
Best Local Similarity   100.0%; Pred. No. 7.2e-115;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

SQ   SEQUENCE   313 AA; 35686 MW; 35BA76D3668B69A3 CRC64;

RESULT 2
Q5TH7 HUMAN
ID   Q5TH7_HUMAN PRELIMINARY;   PRT;   313 AA.
AC   Q5TH7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (Proviral integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;

```
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL353579; CAI20316.1; -; Genomic_DNA.
DR   SMR; Q5T7H7; 32-308.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE 313 AA; 35686 MW; 35BA76D3668E69A3 CRC64;

Query Match             100.0%;  Score 1670;  DB 2;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 7.2e-115;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSK 313
         |||||||||||||
Db   301 EIHLHSLSPGPSK 313


RESULT 3
ID   PIM1_FELCA    STANDARD;    PRT;    313 AA.
AC   Q95LJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
```

OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   Vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.

DR   EMBL; AF259078; AAF67200.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMR; Q9N0P9; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase_1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35630 MW; 9EF40229A847AD47 CRC64;

Query Match   99.2%; Score 1656; DB 1; Length 313;
Best Local Similarity   98.7%;
Matches 309; Conservative   4; Mismatches   0; Indels   0; Gaps   0;
                                   Pred. No. 7.7e-114;

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Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||:||
Db          1 MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENLLIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
              |||||||:||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGPSK 313
              |||||||||||||
Db        301 EIHLHSLSPGPSK 313
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RESULT 5
PIM1_RAT
ID   PIM1_RAT   STANDARD;   PRT;   313 AA.
AC   P26794;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
STRAIN=Sprague-Dawley; TISSUE=Testis;
MEDLINE=92319652; PubMed=1620615;
RA   Wingett D., Reeves R., Magnuson N.S.;
RT   "Characterization of the testes-specific pim-1 transcript in rat.";
RL   Nucleic Acids Res. 20:3183-3189(1992).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.

DR   EMBL; X63675; CAA45214.1; -; mRNA.
DR   PIR; S26298; S26298.
DR   SMR; P26794; 32-308.
DR   Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR   RGD; 3330; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase_1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35631 MW; D5757DA9F1821BF9 CRC64;

Query Match   98.0%; Score 1636; DB 1; Length 313;
Best Local Similarity   97.1%;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;
                                   Pred. No. 2.3e-112;

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Qy          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
              |||||||||||||||||:|:|||:||||||||||||||||||||||||||||||||||:||
Db          1 MLLSKINSLAHLRAAPCSDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENLLIDLNRG 180

Qy        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db
Qy  301 EIHLHSLSPGPSK 313
        ||||||||| |||
Db  301 EIHLHSLSPSPSK 313

Qy  241 PFEHDEEIVKGQVFPRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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RESULT 6
Q8CFN8 MOUSE
ID   Q8CFN8 MOUSE PRELIMINARY;   PRT;   313 AA.
AC   Q8CFN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Proviral integration site 1.
GN   Name=Pim1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX   MEDLINE=22382857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
DR   EMBL; BC042885; AAH42885.1; -; mRNA.
DR   EMBL; BC053019; AAH53019.1; -; mRNA.
DR   EMBL; BC055316; AAH55316.1; -; mRNA.
DR   SMR; Q8CFN8; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.

DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase;
SQ   SEQUENCE   313 AA;   35451 MW;   1294F16A03B7C7D7 CRC64;

Query Match   95.0%;   Score 1587;   DB 2;   Length 313;
Best Local Similarity   94.2%;   Pred. No. 9.3e-109;
Matches 295;   Conservative 10;   Mismatches 8;   Indels 0;   Gaps 0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILLDLNRG 180
        |||||||||||||||||||||:||:|||||||||||||||||||||||||||||||:|||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILLDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIRGQVFPRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
        |||||||| :||||| |:|||||||||:|||:||||||||:||||:|||||| ||||: 
Db  241 PFEHDEEIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGPSK 313
        ||||||||| |||
Db  301 EIHLHSLSPSPSK 313
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RESULT 7
PIM1_MOUSE
ID   PIM1_MOUSE   STANDARD;   PRT;   313 AA.
AC   P06803;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA   Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA   Domen J., van Beveren C., Berns A.;
RT   "The primary structure of the putative oncogene pim-1 shows extensive
RT   homology with protein kinases.";
RL   Cell 46:603-611(1986).
RN   [2]
RP   INTERACTION WITH RP9.
RX   MEDLINE=20389540; PubMed=10931201;
RA   Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA   Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT   "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL   Eur. J. Biochem. 267:5168-5178(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).

CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC   leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; M13945; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1A06.
DR   SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   Proton acceptor (By similarity).
FT   BINDING   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35537 MW; 79F4779E9DCBDC16 CRC64;

Query Match   94.7%;
Best Local Similarity   93.9%;
Matches 294; Conservative   10; Mismatches   9; Indels   0; Gaps   0;
                                Score 1582; DB 1; Length 313;
                                Pred. No. 2.2e-108;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
        |||||||||||||:||||||||||||||| |||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVILL 120
        |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERDSFVILL 120

Qy 121 EREPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||:|||:|||||||||||||||||||||||||||||:||
Db 121 EREPEVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQYFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQTFA 300
        |||||||||:||:||||:|||||||||:|||:|||||||||:|||:||||||||:|||| :
Db 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGPSK 313
        ||||||||||.||
Db 301 EIHLHSLSPGSSK 313

RESULT 8
PIM3_COTJA

ID   PIM3_COTJA   STANDARD;   PRT;   323 AA.
AC   Q9PUB5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=Pim3; Synonyms=Pim-3;
OS   Coturnix coturnix japonica (Japanese quail).

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180181; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AJ130845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot_kinase.
DR   SMART; SM00220; S_TKc; 1.
DR   InterPro; IPR000719; Prot_kinase.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   InterPro; IPR002290; Ser_Thr_Pkinase.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   291   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   168   Proton acceptor (By similarity).
FT   BINDING   69   ATP (By similarity).
SQ   SEQUENCE   323 AA; 36597 MW; E2A4FA20B6F63396C CRC64;

Query Match   68.3%;
Best Local Similarity   67.4%;
Matches 209; Conservative   45; Mismatches   52; Indels   4; Gaps   3;
                                Score 1140; DB 1; Length 323;
                                Pred. No. 8e-76;

Qy   1 MLLSKINSLAHLRAAPCNDLHATKLAP--GKEKEPLESQYQVGPLLGSGGFGSVYSGIRV 58
        |||||.:|||||:.:|.:..|:..||| |:|||||.:.||:||.:||||||.||:|.|
Db   1 MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKEPFDKVYQVGSVLGSGGFGTVYAGSRT 60

Qy   59 SDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVL 118
        :|.|||.|||..|:|:.:|||.|.:.:.||:|||||||||||.||:|||||:||.|.:.
Db   61 ADGLPVAVKHVVKERVTEWGTI-GGVMVPLEIVLLKKVSSGFRGVIKLLDWYERPDGFLI 119

Qy 119 ILEREPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN 178
        :.:||:|:.:|||||||:|||.|:.||.||.|||||||||..|||.||||||||:|:|||
Db 120 VMERPELVKDLFDFITEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDIKDENLLVDLR 179

Qy 179 RGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
        .|||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db 180 TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGILLYDMVCG 239

Qy 239 DIPFEHDEEIIRGQYFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQ 297
        |||||:||||:||:.|||:|:||||.||:||||:|||||||:.:|:.:|.|| :.:.|
Db 240 DIPFEQDEEILRGRLYFRRRISPECQOLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS 299

Qy 298 ETAEIHLHSL 307
        |..:|.|..|
Db 300 EDCDIRLRTL 309

RESULT 9
PIM3_HUMAN

ID   PIM3_HUMAN   STANDARD;   PRT;   326 AA.

AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15540201; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   IDENTIFICATION FROM ESTS.
RX   MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA   Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
RT   "Consistency checks for characterizing protein forms.";
RL   Comput. Biol. Chem. 27:29-35(2003).
CC   -!- FUNCTION: May be involved in cell cycle progression and anti-
CC   apoptosis process. Implicated in proliferation of human hepatoma
CC   cell lines.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC   thymus, and small intestine. Expressed in human hepatoma cell
CC   lines but not in normal liver tissues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AB114795; BAD42438.1; -; mRNA.
DR   EMBL; BC052239; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   170   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 35863 MW; 41FDF9DD2467A162 CRC64;

Query Match
Best Local Similarity   67.8%;   Score 1133; DB 1;   Length 326;
Matches 219; Conservative 35; Mismatches 52; Indels 10; Gaps 7;

Qy   1 MLLSKINSLAHLRAAP--CNDLHATKLIAPGK-EKEPLESQYQVGPLLGSSGGFGSVYSGIR 57
           ||||| ||||| |::|| |||:| :|||| :|:||:||::|.|.:|||:||||
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFGSVGVIRLLLDWFERPDS 115
           ||||: | |:|:| |:|::: :|.||:|||:|:||||||| :|||:|.||.|||||||:|||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy   116 FVLILERPEFVQDLFDFITTERGALQEELARSFFWQVLEAVRHCNCGVLHRDIKDENILI 175
           |:|:|||||:|||||||||||||||:||||||||:|||||||||||||.|||||:||||
Db   119 FLIVLERPEPAQDLFDFITERGALDEPLARRFFRAQVLAAVRHCHSCGVVHRDIKDENLLV 178

Qy   176 DLRNGELKLIDFGSGALLKDTVYTYDFDGTRVYSPSPEWIRYHRYHGRSAAVWSLGTLLYDM 235
           |||||||||||||||||||||:|||||||||||||||||||||||||||||:||.||:||||
Db   179 DLRSGELKLIDFGSGALLKDTVVTFDFDGTRVYSPSPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM--QDV 293
           |||||||:||||||||||||||||||||::|:|::|||:|||||:||:|.:.|:: |||
Db   239 VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG 298

Qy   294 LLPQETAEIHLHSLSP 309
           ||| |:| :|||:|:|
Db   299 GAP-ESCDLRLCTLDP 313

RESULT 10
PIM3_MOUSE

ID   PIM3_MOUSE   STANDARD;   PRT;   326 AA.
AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

```
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; BC017621; AAH17621.1; -; mRNA.
DR   EMBL; BC026639; AAH26639.1; -; mRNA.
DR   HSSP; Q03655; 1HOW.
DR   Ensembl; ENSMUSG00000003828; Mus musculus.
DR   MGI; MGI:1355297; Pim3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    293       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    170              Proton acceptor (By similarity).
FT   BINDING      69              ATP (By similarity).
SQ   SEQUENCE   326 AA;  35970 MW;  DD68C8F46354851E CRC64;

Query Match             67.6%;  Score 1129.5;  DB 1;  Length 326;
Best Local Similarity   72.2%;  Pred. No. 4.8e-75;
Matches  213;  Conservative   31;  Mismatches   44;  Indels    7;  Gaps    5;

Qy    1 MLLSKINSLAHLRRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLCGSGGFGSVYSGIR 57
        |||||   |||||||||  | |||||| |||| |||| |||  ||||| ||||||||| |||
Db    1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
        ||.|||||||||||||.|| | || ||||||||  |.|  ||| ||| ||||.||||||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy  116 FVIILEREPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLI 175
        |:||||| ||||||||||||||||||  ||| ||||| ||||||||||||||||||||:|
Db  119 FLIVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy  176 DLNRGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
        ||. ||||||||.|||.|||||.|||||| ||||||||||||||||||.||||||||||
Db  179 DLRSGELKLIDFGSGAVLKDTVVTDFDGTRVSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy  236 VCGDIPFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWM 290
        ||||||| |||| |||| | | ||| || |||  |||||||:|||| |||| |||
Db  239 VCGDIPFEQDEEILRGRLFFRRVSPECCQLIEWCLSLRPSERPSLDQIAAHPWM 293
```

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RESULT 11
PIM3_RAT
ID   PIM3_RAT      STANDARD;      PRT;   326 AA.
AC   O70444;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE   Kid-1) (Kinase induced by depolarization).
GN   Name=Pim3; Synonyms=Kid1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Konietzko U., Kuhl D.;
RT   "Pim-3 is a member of the pim kinase family.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX   MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA   Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA   Bazan N.G., Baudry M., Herschman H.R.;
RT   "KID-1, a protein kinase induced by depolarization in brain.";
RL   J. Biol. Chem. 273:16535-16543(1998).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC       including brain.
CC   -!- INDUCTION: By membrane depolarization or forskolin.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF086624; AAC68900.1; ALT_INIT; mRNA.
DR   EMBL; AF057026; AAC36065.1; -; mRNA.
DR   HSSP; Q03655; 1HOW.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; IDA.
DR   GO; GO:0016572; P:histone phosphorylation; IDA.
DR   RGD; 620462; Pim3.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    293       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    170              Proton acceptor (By similarity).
FT   BINDING      69              ATP (By similarity).
SQ   SEQUENCE   326 AA;  36002 MW;  DD6C98F4635F851E CRC64;

Query Match             67.6%;  Score 1128.5;  DB 1;  Length 326;
Best Local Similarity   72.2%;  Pred. No. 5.7e-75;
Matches  213;  Conservative   31;  Mismatches   44;  Indels    7;  Gaps    5;

Qy    1 MLLSKINSLAHLRRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLCGSGGFGSVYSGIR 57
        |||||   |||||||||  | |||||| |||| |||| |||  ||||| ||||||||| |||
Db    1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
        ||.|||||||||||||.|| | || ||||||||  |.|  ||| ||| ||||.||||||
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy  116 FVIILEREPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLI 175
        |:||||| ||||||||||||||||||  ||| ||||| ||||||||||||||||||||:|
Db  119 FLIVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178
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RESULT 12

Qy   176  DLNRGELKLIDFGCSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
              |||.||||||||| ||.|||||||||||||||||||||||||||||||.||||||.|||||
Db   179  DLRSGELKLIDFGGSGAVLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
              ||||||| |||| || ..|||.|||.||| ||.||.||.|||.||..|..|.||  |||
Db   239  VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 293
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ID   Q4V8M2_RAT     PRELIMINARY;      PRT;    380 AA.
AC   Q4V8M2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC097317; AAH97317.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER          1      1
SQ   SEQUENCE   380 AA;  41568 MW;  F82BBE50DD71346 CRC64;
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Query Match             67.6%;  Score 1128.5;  DB 2;  Length 380;
Best Local Similarity   72.8%;  Pred. No. 6.6e-75;
Matches  213;  Conservative  31;  Mismatches  44;  Indels  7;  Gaps  5;
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Qy   236  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
              ||||||| |||| || ..|||.|||.||| ||.||.||.|||.||..|..|.||  |||
Db   233  VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 347
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RESULT 13

Qy     1  MLLSKINSLAHLRAAP--CNDLHATKLAPGK-EKEPLESQYQVGPLLGSSGGFGSVYSGIR 57
              |||||||||||||||    ||| | || ||| |||||||||||||||||||||||||||||
Db     1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKYYQVGAVLGSSGGFGTVYAGSR 59

Qy    58  VSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
              ::|||||||.|.||||||:||.|||||.|.|||||||.   |||||||||||||||||||
Db    60  IADGLPVAVHVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 115

Qy   116  FVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLI 175
              |:|:||||:|.|||||||||||||.|||||||.||| |||||||||||||:||||||||:
Db   119  FLLVLERPEPAQDLFDFITERGALDEPLARRFAQVLAAVRHCHNCGVVHRDIKDENLLV 178
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ID   Q811X8_MOUSE   PRELIMINARY;      PRT;    325 AA.
AC   Q811X8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   KID1.
GN   Name=Pim3; Synonyms=Kid1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu L.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AY026239; AAK16606.1; -; mRNA.
DR   HSSP; Q03656; 1Q99.
DR   SMR; Q811X8; 36-292.
MGI; MGI:1355297; Pim3.
GO   GO; GO:0005524; F:ATP binding; IEA.
GO   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   325 AA;  35931 MW;  77DEF8820F41E3F4 CRC64;
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Query Match             66.8%;  Score 1116;  DB 2;  Length 325;
Best Local Similarity   71.9%;  Pred. No. 4.7e-74;
Matches  212;  Conservative  32;  Mismatches  43;  Indels  8;  Gaps  6;
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Qy   176  DLNRGELKLIDFGSGALLKDTVTFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   179  DLRSGELKLIDFGSGAVLKDTVYTFDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236  VCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM 290
          |||||||||||||||||||||||||||||||||||||||||||||
Db   239  VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSRPSERPSLDKL-CHPWM 292

RESULT 14
PIM3_XENLA
ID   PIM3_XENLA          STANDARD;      PRT;   323 AA.
AC   Q91822;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN   Name=PIM3; Synonyms=PIM1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RX   MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
RA   Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
RA   Aebersold R., Pelech S.L.;
RT   "Identification of the autophosphorylation sites of the Xenopus laevis
RT   Pim-1 proto-oncogene-encoded protein kinase.";
RL   J. Biol. Chem. 272:10514-10521(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC       represent the pim-3 isoform.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; L29495; AAA85389.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    291       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    168    168       Proton acceptor (By similarity).
FT   BINDING      69     69       ATP (By similarity).
FT   MOD_RES       4      4       Phosphoserine (by autocatalysis)
FT                                (partial).
FT   MOD_RES     190    190       Phosphoserine (by autocatalysis).
FT   MOD_RES     205    205       Phosphothreonine (by autocatalysis)
FT                                (partial).
SQ   SEQUENCE   323 AA;  36964 MW;  AB4DD61E7A99A38F CRC64;

Query Match             66.2%;  Score 1105;  DB 1;  Length 323;
Best Local Similarity   65.3%;  Pred. No. 3e-73;
Matches  205;  Conservative  47;  Mismatches  50;  Indels  12;  Gaps  5;

Qy     1  MLLSKINSLAHLRAAPCN------------DLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
          |||||:||||:||:                 :|: ||| : :|    ::  ::||||||||||||
Db     1  MLLSKFGSLAHI----CNPSNMEHLPVKILQPVVDKEPFEKYQVGSVVASGGFGTVYS 56
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Qy    55  GIRVSDNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPD 114
          |:|| |   ||||:|:|||:||||||||||||||:||||||||||||:||||||||||||
Db    57  DSRIADGQPVAVKHVAKERVTEWGTL-NGVMVPLEIVLLKKVPFAFRGVINLLDWYERPD 115

Qy   115  SFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIL 174
          ||:||||::|| ||||| ||||||| :: || ||||||||||||||||||||||||||||
Db   116  AFLIVMEREPPVKDLFDYITEKGPILEDTARGFFRQVLEAVRHCYNCGVVHRDIKDENLL 175

Qy   175  IDLNRGELKLIDFGSGALLKDTVTFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYD 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   176  VDTRNGELKLIDFGSGAVLKDTVYTFDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYD 235

Qy   235  MVCGDIPFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDV 293
          ||||||||:|||| ||:|||||:|||:||| ||:|||| |||:|||: :|:| : |:
Db   236  MVYGDIPFEQDEEIVRRLCFRRRISTECQQLIKWCLSRPSDRPTLEQIFDHPWMCKCD 295

Qy   294  LLPQETAEIHLHSL 307
          |||:||| || ||
Db   296  LVKSEDCDLRLRTI 309

RESULT 15
Q66I11_XENTR
ID   Q66I11_XENTR PRELIMINARY;      PRT;   318 AA.
AC   Q66I11;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Pim3-prov protein.
GN   Name=pim3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RC   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RL   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC081340; AAH81340.1; -; mRNA.
DR   SMR; Q66I11; 32-297.
DR   Ensembl; ENSXETG00000009354; Xenopus tropicalis.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
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DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   318 AA;  36547 MW;  48CCF12797F01FDC CRC64;

Query Match      65.9%;  Score 1101;  DB 2;  Length 318;
Best Local Similarity   70.3%;  Pred. No. 5.9e-73;
Matches  204;  Conservative  38;  Mismatches  38;  Indels  10;  Gaps  4;

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Qy    70 EKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDL 129
            :|||    |  ||||:| |||||||:|| | |||||||||:||||||| |:|||||||||
Db    69 SRDRIGEMKHM-NGTLVPLEIYLLKKVSNGCRGVIRLLDWYERPDGFIIIMERPEPVQDL 127

Qy   130 FDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGS 189
            |||||||||| |||| ||| ||:|||||||:|| :|||||||||||:||  |||||||||
Db   128 FDFITERGALGEELATNFFRQVVEAVRHCHSCDVVHRDIKDENILVDLRTAELKLIDFGS 187

Qy   190 GALLKDTVYTDFDFGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEII 249
            ||||:| ||||||:|||||||||||:| ||||||| |||||||||||||||||||||:|| :
Db   188 GALLRDAVYTDFDPGTRVYSPPEWIRFHXYHGRSATVWSLGILLYDMVCGDIPFEHDDEIL 247

Qy   250 RGQVFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWM-QDVLLPQE 298
            :| : | :|| ||||||:||| :||||||| |||| :|||| ||  |
Db   248 KGKIQYRCRVSRECQHLIEWCLSKRPSDRPSLEQILAHPWMSQDNFLDKK 297

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OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: May 4, 2006, 05:25:14 ; Search time 28.6667 Seconds
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Title: US-10-705-757-4
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	2	US-09-237-543-8	Sequence 8, Appli
2	1668	100.0	313	2	US-09-644-450-8	Sequence 8, Appli
3	1636	98.1	313	2	US-09-237-543-9	Sequence 9, Appli
4	1636	98.1	313	2	US-09-644-450-9	Sequence 9, Appli
5	1623	97.3	313	1	US-08-463-081B-26	Sequence 26, Appl
6	1623	97.3	313	1	US-08-461-379A-26	Sequence 26, Appl
7	1623	97.3	313	1	US-08-462-390B-26	Sequence 26, Appl
8	1623	97.3	313	1	US-08-463-074B-26	Sequence 26, Appl
9	1623	97.3	313	2	US-08-465-585C-26	Sequence 26, Appl
10	1623	97.3	313	2	US-08-652-44-26	Sequence 26, Appli
11	1584	95.0	313	2	US-09-237-543-7	Sequence 7, Appli
12	1584	95.0	313	2	US-09-644-450-7	Sequence 7, Appli
13	1304.5	78.2	257	1	US-07-857-224B-41	Sequence 41, Appl
14	1135	68.0	326	2	US-09-237-543-2	Sequence 2, Appl
15	1135	68.0	326	2	US-09-644-450-2	Sequence 2, Appli
16	1131.5	67.8	455	2	US-09-237-543-5	Sequence 5, Appli
17	1131.5	67.8	455	2	US-09-644-450-5	Sequence 5, Appli
18	1102.5	66.1	323	2	US-09-237-543-6	Sequence 6, Appli
19	1102.5	66.1	323	2	US-09-644-450-6	Sequence 6, Appli
20	1083.5	65.0	254	2	US-09-237-543-4	Sequence 4, Appli
21	1083.5	65.0	254	2	US-09-644-450-4	Sequence 4, Appli
22	866.5	51.9	311	2	US-09-184-563-2	Sequence 2, Appli
23	866.5	51.9	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	378.5	22.7	256	2	US-09-964-956-74	Sequence 74, Appl
25	376.5	22.6	778	2	US-10-116-326-2	Sequence 2, Appli
26	376.5	22.6	778	2	US-10-003-690-2	Sequence 2, Appli
27	376.5	22.6	778	2	US-10-803-277-2	Sequence 2, Appli
28	374	22.4	1101	2	US-09-770-170-8	Sequence 8, Appli
29	370.5	22.2	776	2	US-09-523-849-34	Sequence 34, Appl
30	366	21.9	1356	2	US-09-770-170-6	Sequence 6, Appli
31	364.5	21.9	630	2	US-10-355-975A-38	Sequence 38, Appl
32	364.5	21.9	630	2	US-09-579-664R-11	Sequence 11, Appl
33	364.5	21.9	631	2	US-10-355-975A-11	Sequence 11, Appl
34	363.5	21.8	1323	2	US-09-770-170-2	Sequence 2, Appli
35	357.5	21.4	668	2	US-09-930-181-2	Sequence 2, Appli
36	357.5	21.4	668	2	US-10-283-247-2	Sequence 2, Appli
37	357.5	21.4	674	2	US-09-633-328B-4	Sequence 4, Appli
38	357	21.4	512	2	US-10-054-579-2	Sequence 2, Appli
39	356	21.3	281	2	US-09-633-328B-2	Sequence 2, Appli
40	355.5	21.3	256	2	US-10-248-796A-20512	Sequence 20512, A
41	353.5	21.2	674	2	US-09-633-328B-2	Sequence 2, Appli
42	353.5	21.2	674	2	US-10-283-247-7	Sequence 7, Appli
43	353.5	21.2	674	2	US-10-283-247-8	Sequence 8, Appli
44	343.5	20.6	722	2	US-08-817-832B-32	Sequence 32, Appli
45	343	20.6	1005	2	US-09-770-170-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-237-543-8
; Sequence 6, Application US/0927543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match   100.0%; Score 1668; DB 2; Length 313;
Best Local Similarity   100.0%; Pred. No. 1.4e-164;
Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
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Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
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Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
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Db  181  ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
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Db  241  PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy  301  EIHLHSLSPSPSK  313
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Db  301  EIHLHSLSPSPSK  313
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RESULT 2
US-09-644-450-8

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; Sequence 8, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-644-450-8

  Query Match         100.0%;  Score 1668;  DB 2;  Length 313;
  Best Local Similarity   100.0%;
  Matches 313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
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Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
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Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy 301 EIHLHSLSPSPSK  313
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Db 301 EIHLHSLSPSPSK  313


RESULT 3
US-09-237-543-9
; Sequence 9, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-237-543-9

  Query Match          98.1%;  Score 1636;  DB 2;  Length 313;
  Best Local Similarity    97.1%;
  Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
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Db   1 MLLSKINSLAHLRRAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
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Db 241 PFEHDEEIIRGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy 301 EIHLHSLSPSPSK  313
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Db 301 EIHLHSLSPSPSK  313


RESULT 4
US-09-644-450-9
; Sequence 9, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-450-9

  Query Match          98.1%;  Score 1636;  DB 2;  Length 313;
  Best Local Similarity    97.1%;
  Matches 304;  Conservative  6;  Mismatches  3;  Indels  0;  Gaps  0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
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Db   1 MLLSKINSLAHLRRAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
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Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
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Db 241 PFEHDEEIIRGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy 301 EIHLHSLSPSPSK  313
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Db 301 EIHLHSLSPSPSK  313


RESULT 5
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; Patent No. 5871960
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Left column:

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; Patent No. 5871960 5837487
; GENERAL INFORMATION:
;   APPLICANT: Smith, Kendall A. & Beadling, Carol
;   TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
;   TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;     STREET: 444 South Flower St. - Suite 1900
;     CITY: Los Angeles
;     STATE: California
;     COUNTRY: USA
;     ZIP: 90071
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0,
;     SOFTWARE: Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/463,081B
;     FILING DATE: 5-JUN-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/104,736
;     FILING DATE: 10-AUG-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 07/796,066
;     FILING DATE: 20-NOV-91
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Viviana Amzel, Ph. D.
;     REGISTRATION NUMBER: 30,930
;     REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (213) 622-7700
;     TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 313 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: n.a.
;     TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-463-081B-26

Query Match                97.3%;  Score 1623;  DB 1;  Length 313;
Best Local Similarity      96.5%;  Pred. No. 6.7e-160;
Matches 302;  Conservative   6;  Mismatches   5;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db      1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
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Db    181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
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Db    301 EIHLHSLSPGPSK 313
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Right column:

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RESULT 6
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
;   APPLICANT: Smith, Kendall A. & Beadling, Carol
;   TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
;   TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
;   TITLE OF INVENTION: Expression Thereof
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Ratner & Prestia
;     STREET: One Westlakes-Berwyn   (B)
;     CITY: Valley Forge
;     STATE: Pennsylvania
;     COUNTRY: USA
;     ZIP: 19482
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0,
;     SOFTWARE: Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/461,379A
;     FILING DATE: 5-JUNE-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: USSN 08/330,108; 08/104,736
;     APPLICATION NUMBER: & 07/796,066
;     FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Viviana Amzel, Ph. D.
;     REGISTRATION NUMBER: 30,930
;     REFERENCE/DOCKET NUMBER: DART-070
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (610)470-0700
;     TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 313 amino acids
;     TYPE: peptide
;     STRANDEDNESS: n.a.
;     TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-461-379A-26

Query Match                97.3%;  Score 1623;  DB 1;  Length 313;
Best Local Similarity      96.5%;  Pred. No. 6.7e-160;
Matches 302;  Conservative   6;  Mismatches   5;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db      1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
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Db    181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy    301 EIHLHSLSPGPSK 313
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Db    301 EIHLHSLSPGPSK 313
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RESULT 7
US-08-462-390B-26
Sequence 26, Application US/08462390B
Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A.; & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,390B
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)407-0700
; TELEFAX: (610)407-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-462-390B-26

Query Match   97.3%; Score 1623; DB 1; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
Matches 302; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVVSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFPRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
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Db 301 EIHLHSLSPGPSK 313

RESULT 8
US-08-463-074B-26
Sequence 26, Application US/08463074B
Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,074B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-463-074B-26

Query Match   97.3%; Score 1623; DB 2; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
Matches 302; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVVSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
         |||||||| ||| :|||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIRGQVFPRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
         |||||||||| ||
Db 301 EIHLHSLSPGPSK 313

Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
       |||||||| |||
Db 301 EIHLHSLSPGPSK 313

RESULT 9
US-08-465-585C-26
; Patent No. 6027914
; Sequence 26, Application US/08465585C
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 190
; CITY: Los Angeles
; STATE: Californiaa
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,585C
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489210
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide

US-08-465-585C-26

Query Match   97.3%; Score 1623; DB 2; Length 313;
Best Local Similarity   96.5%; Pred. No. 6.7e-160;
Matches 302; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
        ||||||||||||||:|||||||||:|||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFPSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERREPVQDLFDIITERGALQEELARSFPWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db 121 ERREPVQDLFDIITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQETA 300
        |||||||: ||||||||||||||||||||| ||||||| |||||||||||||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
        |||||||| |||
Db 301 EIHLHSLSPGPSK 313

RESULT 10
US-08-652-446-26
; Sequence 26, Application US/08652446
; Patent No. 6057427
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5
; TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESSEE: (B) STREET: 444 South Flower St. - Suite 190
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,446
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP App. # 96921319.8
; FILING DATE: 5-JAN-1998
; APPLICATION NUMBER: PCT/US/96/09194
; FILING DATE: 5-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: 08/462,337
; FILING DATE: 5-JUN-1995
; APPLICATION NUMBER: 08/462,390
; FILING DATE: 5-JUN-1995
; APPLICATION NUMBER: 08/465,585
; FILING DATE: 5-JUN-1995
; APPLICATION NUMBER: 08/463,074
; FILING DATE: 5-JUN-1995
; APPLICATION NUMBER: 08/463,081
; FILING DATE: 5-JUN-1995
; APPLICATION NUMBER: 08/461,379
; FILING DATE: 5-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/739,523
; FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 40035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:

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;  SEQUENCE CHARACTERISTICS:
;     LENGTH:  313 amino acids
;     TYPE:  peptide
;     STRANDEDNESS:  n.a.
;     TOPOLOGY:  n.a.
;     MOLECULE TYPE:  peptide
US-08-652-446-26

Query Match             97.3%;  Score 1623;  DB 2;  Length 313;
Best Local Similarity   96.5%;  Pred. No. 6.7e-160;
Matches 302;  Conservative 6;  Mismatches 5;  Indels 0;  Gaps 0;

Qy      1  MLLSKINSLAHLRAAPACNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
           ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120

Qy    121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHMMQDVLLPQATA  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db    241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLARPSDRPTFEEIQNHPMMQDVLLPQETA  300

Qy    301  EIHLHSLSPSPSK 313
           |||||||||||||
Db    301  EIHLHSLSPGPSK 313


RESULT 11
US-09-237-543-7
;  Sequence 7, Application US/09237543A
;  Patent No. 6143540
;  GENERAL INFORMATION:
;     APPLICANT:  Kapeller, Rosana
;     TITLE OF INVENTION:  NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;     TITLE OF INVENTION:  AND USES THEREOF
;     FILE REFERENCE:  035800/175631
;     CURRENT APPLICATION NUMBER:  US/09/237,543A
;     CURRENT FILING DATE:  1999-01-26
;     NUMBER OF SEQ ID NOS:  11
;     SOFTWARE:  Patentin Ver. 2.0
;  SEQ ID NO 7
;     LENGTH:  313
;     TYPE:  PRT
;     ORGANISM:  Mus musculus
US-09-237-543-7

Query Match             95.0%;  Score 1584;  DB 2;  Length 313;
Best Local Similarity   94.2%;  Pred. No. 7.5e-156;
Matches 295;  Conservative 8;  Mismatches 10;  Indels 0;  Gaps 0;

Qy      1  MLLSKINSLAHLRAAPACNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
           ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120
           ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120

Qy    121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
           |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180

Qy    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHMMQDVLLPQATA  300
           |||||||||:|||:|||||||||||||||||:|||||||||:||||||||||||||||:
Db    241  PFEHDEEIIKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS  300

Qy    301  EIHLHSLSPSPSK 313
           |||||||||:||
Db    301  EIHLHSLSPGSSK 313


RESULT 12
US-09-644-450-7
;  Sequence 7, Application US/09644450
;  Patent No. 6383791
;  GENERAL INFORMATION:
;     APPLICANT:  Kapeller, Rosana
;     TITLE OF INVENTION:  NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;     TITLE OF INVENTION:  AND USES THEREOF
;     FILE REFERENCE:  035800/175631
;     CURRENT APPLICATION NUMBER:  US/09/644,450
;     CURRENT FILING DATE:  2000-08-23
;     NUMBER OF SEQ ID NOS:  11
;     SOFTWARE:  Patentin Ver. 2.0
;  SEQ ID NO 7
;     LENGTH:  313
;     TYPE:  PRT
;     ORGANISM:  Mus musculus
US-09-644-450-7

Query Match             95.0%;  Score 1584;  DB 2;  Length 313;
Best Local Similarity   94.2%;  Pred. No. 7.5e-156;
Matches 295;  Conservative 8;  Mismatches 10;  Indels 0;  Gaps 0;

Qy      1  MLLSKINSLAHLRAAPACNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
           ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120
           ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120

Qy    121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
           |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180

Qy    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHMMQDVLLPQATA  300
           |||||||||:|||:|||||||||||||||||:|||||||||:||||||||||||||||:
Db    241  PFEHDEEIIKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS  300

Qy    301  EIHLHSLSPSPSK 313
           |||||||||:||
Db    301  EIHLHSLSPGSSK 313


RESULT 13
US-07-857-224B-41
;  Sequence 41, Application US/07857224B
;  Patent No. 5958784
;  GENERAL INFORMATION:
;     APPLICANT:  Benner, Steven A.
;     TITLE OF INVENTION:  Predicting Folded Structures of Proteins
;     NUMBER OF SEQUENCES:  114
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE:  Steven A. Benner
;        STREET:  Hadlaubstrasse 151
;        CITY:  Zurich
;        STATE:  none
```

```
;  COUNTRY: Switzerland
;  ZIP: (note: this is an international post code) CH-8092
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
;  COMPUTER: Apple Macintosh
;  OPERATING SYSTEM: Macintosh 7.0
;  SOFTWARE: Microsoft Word
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/857,224B
;  FILING DATE: 03/25/92
;  CLASSIFICATION: 436
;  PRIOR APPLICATION DATA: none
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (international) 41 1 632 2830
;  TELEFAX: (international) 41 1 262 2437
;  TELEX: none
;  SEQUENCE CHARACTERISTICS:
;  INFORMATION FOR SEQ ID NO: 41:
;  LENGTH: 257
;  TYPE: amino acid
;  TOPOLOGY: linear
;  MOLECULE TYPE:
;  TYPE: protein
;  DESCRIPTION: protein
;  ORIGINAL SOURCE:
;  ORGANISM: rat
;  FEATURE: Protein kinase; Table 8 Column 46
;  PUBLICATION INFORMATION:
;  AUTHORS:
;  AUTHORS: Hanks, S. K.
;  AUTHORS: Quinn, A. M.
;  AUTHORS: Hunter, T.
;  TITLE: The protein kinase family
;  JOURNAL: Science
;  VOLUME: 241
;  PAGES: 42-52
;  DATE: 1988
;  US-07-857-224B-41

Query Match    78.2%;  Score 1304.5;  DB 1;  Length 257;
Best Local Similarity   94.9%;  Pred. No. 5.6e-127;
Matches  244;  Conservative  7;  Mismatches  3;  Indels  3;  Gaps  2;

Qy   36  SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKK  95
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1  SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVPMEVVLLKK  58

Qy   96  VSSGFSGVIRLLDDWFERPDSFVLILEREPEVQDLFDFITERGALQEELARSFFWQVLEAV  155
         ||| |||||||||||||||||||||||||||||||||||||||||||| ||| |||||||
Db   59  VSSDFSGVIRLLDDWFERPDSFVLILERPEPEVQDLFDFITERGALQEDLLARGFFWQVLEAV  118

Qy  156  RICHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRY  215
         ||||||||||||||||||||||:||||||||||||||||||||||:||||||||||||||
Db  119  RICHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVTFDFDGTRVSYSPPEWIRY  178

Qy  216  HRYHGRSAAVWSLGILLYDMVCGDIPF-EHDEEIVKGQVYFRQRVSSECQHLIRWCLSLR  274
         ||||||||||||||||||||||||||| ||||||:||||:|||:|||||||||:|||||||
Db  179  HRYHGRSAAVWSLGILLYDMVCGDIPFDEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLR  238

Qy  275  PSDRPSFEEIQNHPWMQ  291
         ||||||||||:||||||
Db  239  PSDRPSFEEIRNHPWMQ  255
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;  CURRENT FILING DATE: 1999-01-26
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 2
;  LENGTH: 326
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  US-09-237-543-2

Query Match    68.0%;  Score 1135;  DB 2;  Length 326;
Best Local Similarity   69.6%;  Pred. No. 3.1e-109;
Matches  220;  Conservative  34;  Mismatches  52;  Indels  10;  Gaps  7;

Qy    1  MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
         |||||  |||||       ||| || |  ||  | ||| ||||||||||||||||||||||
Db    1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGPLLGSGGFGSVYSGIR  59

Qy   58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDDWFERPDS  115
         :||:|||| |||| :  | |||  |   |:|:|:| ||  :| : ||:|||||||||||
Db   60  IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDDWFERPDG  118

Qy  116  FVLILEREPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI  175
         ||||||| || ||||||||||||| | ||| ||  ||| ||||| ||| |||||||| |
Db  119  FVLILERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178

Qy  176  DLNRGELKLIDFGSGALLKDTVYTDFDGTRVSYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
         || :||||||||||||||||||:||||||||||||||||||||||||||:||||||:||||
Db  179  DLRSGELKLIDFGSGALLKDTVTFDFDGTRVSYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy  236  VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRSDRPSFEEIQNHPWM--QDV  293
         |||||||| |||: : | ||| |||||||||||||||| : ||:  | :||||  ||:
Db  239  VCGDIPFEQDEEILRGRLFRRRVSPECQHLIRWCLSLRPSERPSLDDIAAHPWMLGADG  298

Qy  294  LLPQATAEIHLHSLSP  309
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Db  299  GAPE-SCDLRLCTLDP  313
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RESULT 15
US-09-644-450-2
Sequence 2, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
;  APPLICANT: Kapeller, Rosana
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 035800/175631
;  CURRENT APPLICATION NUMBER: US/09/644,450
;  CURRENT FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 11
;  SEQ ID NO 2
;  SOFTWARE: Patentin Ver. 2.0
;  LENGTH: 326
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  US-09-644-450-2

Query Match    68.0%;  Score 1135;  DB 2;  Length 326;
Best Local Similarity   69.6%;  Pred. No. 3.1e-109;
Matches  220;  Conservative  34;  Mismatches  52;  Indels  10;  Gaps  7;

Qy    1  MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
         |||||  |||||       ||| || |  ||  | ||| ||||||||||||||||||||
Db    1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGPLLGSGGFGSVYTAGSR  59

Qy   58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDDWFERPDS  115
         :||:|||| |||| :  | |||  |   |:|:|:| ||  :| : ||:|||||||||||||
Db   60  IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDDWFERPDG  118

Qy  116  FVLILEREPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI  175
         ||||||| || ||||||||||||| | ||| ||  ||| ||||| ||| |||||||| |:
Db  119  FVLILERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178
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```
RESULT 14
US-09-237-543-2
Sequence 2, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
;  APPLICANT: Kapeller, Rosana
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 035800/175631
;  CURRENT APPLICATION NUMBER: US/09/237,543A
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Qy   176  DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
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Db   179  DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy   236  VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM--QDV  293
          |||||||||||:::::||:::  ||||||:|  :||  ||| |||    |||  QDV
Db   239  VCGDIPFEQDEEILRGRLLFRRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADG  298

Qy   294  LLPQATAEIHLHSLSP  309
          |:  :::|  |:|  |
Db   299  GAPE-SCDLRLCTLDP  313
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OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: May 4, 2006, 05:26:13 ; Search time 92.6667 Seconds
(without alignments)
1411.301 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL............LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	3	US-09-971-791-8	Sequence 8, Appli
2	1668	100.0	313	4	US-10-348-081-12	Sequence 12, Appli
3	1668	100.0	313	3	US-10-705-757-4	Sequence 4, Appli
4	1636	98.1	313	3	US-09-971-791-9	Sequence 9, Appli
5	1636	98.1	313	4	US-10-081-119-18	Sequence 18, Appli
6	1636	98.1	313	4	US-10-394-322A-52	Sequence 52, Appli
7	1636	98.1	313	4	US-10-348-081-13	Sequence 13, Appli
8	1636	98.1	313	3	US-10-705-757-1	Sequence 1, Appli
9	1636	98.1	313	4	US-10-664-421-1	Sequence 1, App
10	1636	98.1	313	4	US-10-664-421-150	Sequence 150, App
11	1636	98.1	313	3	US-10-705-757-2	Sequence 2, Appli
12	1636	98.1	313	4	US-10-377-268-9	Sequence 9, Appli
13	1636	98.1	313	4	US-10-951-389-18	Sequence 18, Appli
14	1636	98.1	313	5	US-10-951-406-18	Sequence 18, Appli
15	1636	98.1	313	5	US-10-951-477-18	Sequence 18, Appli
16	1636	98.1	313	5	US-10-977-087-18	Sequence 18, Appli
17	1636	98.1	313	5	US-10-941-635-152	Sequence 152, Appl
18	1623	97.3	313	3	US-10-620-052A-22	Sequence 22, Appl
19	1584	95.0	313	3	US-09-971-791-7	Sequence 7, Appli
20	1584	95.0	313	4	US-10-348-081-14	Sequence 14, Appli
21	1584	95.0	313	4	US-10-081-119-14	Sequence 14, Appli
22	1584	95.0	313	3	US-10-705-757-6	Sequence 6, Appli
23	1584	95.0	313	4	US-10-377-268-10	Sequence 10, Appli
24	1584	95.0	253	4	US-10-941-635-12	Sequence 2, Appli
25	1345	80.6	323	4	US-10-620-052A-71	Sequence 71, Appli
26	1137	68.2	323	4	US-10-664-421-7	Sequence 7, Appli
27	1137	68.2	323	4	US-10-377-268-15	Sequence 15, Appli
28	1137	68.2	323	5	US-10-941-635-7	Sequence 7, Appli
29	1137	68.2	374	5	US-11-425-114-54275	Sequence 54275, A
30	1135	68.0	374	3	US-09-971-791-2	Sequence 2, Appli
31	1135	68.0	326	4	US-10-348-081-2	Sequence 2, Appli
32	1135	68.0	326	4	US-10-664-421-166	Sequence 166, App
33	1135	68.0	326	4	US-10-618-941-82	Sequence 82, Appl
34	1135	68.0	374	5	US-11-425-114-54264	Sequence 54264, A
35	1132.5	67.9	326	4	US-10-425-114-54275	Sequence 6, Appl
36	1132.5	67.9	326	4	US-10-348-081-6	Sequence 6, Appl
37	1132.5	67.9	326	4	US-10-705-757-11	Sequence 11, Appl
38	1132.5	67.9	326	4	US-10-377-268-14	Sequence 14, Appl
39	1131.5	67.8	326	4	US-10-941-635-6	Sequence 6, Appli
40	1131.5	67.8	455	3	US-09-971-791-5	Sequence 5, Appli
41	1131.5	67.8	455	4	US-10-348-081-10	Sequence 10, Appli
42	1119	67.1	325	4	US-10-664-421-21	Sequence 5, Appli
43	1102.5	66.1	323	3	US-09-971-791-6	Sequence 6, Appli
44	1102.5	66.1	323	4	US-10-348-081-11	Sequence 11, Appli
45	1102.5	66.1	323	4	US-10-664-421-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-971-791-8
; Sequence 8, Application US/09971791
; Patent No. US2002011520A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-971-791-8

Query Match   100.0%; Score 1668; DB 3; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSIGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db    241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy    301 EIHLHSLSPSPSK 313
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Db    301 EIHLHSLSPSPSK 313
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Db   301 EIHLHSLSPSPSK 313

RESULT 2
US-10-348-081-12
; Sequence 12, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 12
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-348-081-12

Query Match   100.0%; Score 1668; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPSPSK 313
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Db 301 EIHLHSLSPSPSK 313

RESULT 3
US-10-705-757-4
; Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-10-705-757-4

Query Match   100.0%; Score 1668; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPSPSK 313
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Db 301 EIHLHSLSPSPSK 313

RESULT 4
US-09-971-791-9
; Sequence 9, Application US/09971791
; Patent No. US20020015120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-791-9

Query Match   98.1%; Score 1636; DB 3; Length 313;
Best Local Similarity 97.1%; Pred. No. 4.7e-140;
Matches 304; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

RESULT 5
US-10-081-119-18
Sequence 18, Application US/10081119
Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TYK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Query Match   98.1%;   Score 1636; DB 4; Length 313;
Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
Matches   304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVAD   60
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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVSD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 6
US-10-394-322A-52
Sequence 52, Application US/10394322A
Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A

Query Match   98.1%;   Score 1636; DB 4; Length 313;
Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
Matches   304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVAD   60
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Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVSD   60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

RESULT 7
US-10-348-081-13
Sequence 13, Application US/10348081
Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-348-081-13

Query Match   98.1%;   Score 1636; DB 4; Length 313;
Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
Matches   304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGGFGSVSYSGIRVAD   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
           |||||||||||||
Db   301 EIHLHSLSPGPSK 313

```
Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILIDLNRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPSPSK  313
         ||||||||||||
Db  301  EIHLHSLSPGPSK  313
```

RESULT 8
US-10-664-421-1

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; Sequence 1, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
;  APPLICANT: BREMER, RYAN
;  APPLICANT: IBRAHIM, PRABHA
;  APPLICANT: KUMAR, ABHINAV
;  APPLICANT: MANDIYAN, VALSAN
;  APPLICANT: MILBURN, MICHAEL V.
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
;  FILE REFERENCE: 039363/0703
;  CURRENT APPLICATION NUMBER: US/10/664,421
;  CURRENT FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: 60/412,341
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: 60/411,398
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 169
;  SOFTWARE: Patentin Ver. 3.2
;
;  SEQ ID NO 1
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-664-421-1

  Query Match       98.1%;   Score 1636;  DB 4;  Length 313;
  Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
  Matches  304;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         |||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILIDLNRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPSPSK  313
         ||||||||||||
Db  301  EIHLHSLSPGPSK  313
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RESULT 9

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US-10-664-421-150
; Sequence 150, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
;  APPLICANT: BREMER, RYAN
;  APPLICANT: IBRAHIM, PRABHA
;  APPLICANT: KUMAR, ABHINAV
;  APPLICANT: MANDIYAN, VALSAN
;  APPLICANT: MILBURN, MICHAEL V.
;  TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
;  FILE REFERENCE: 039363/0703
;  CURRENT APPLICATION NUMBER: US/10/664,421
;  CURRENT FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: 60/412,341
;  PRIOR FILING DATE: 2002-09-20
;  PRIOR APPLICATION NUMBER: 60/411,398
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 169
;  SOFTWARE: Patentin Ver. 3.2
;
;  SEQ ID NO 150
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-664-421-150

  Query Match       98.1%;   Score 1636;  DB 4;  Length 313;
  Best Local Similarity   97.1%;   Pred. No. 4.7e-140;
  Matches  304;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         |||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILIDLNRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLILIDLNRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPSPSK  313
         ||||||||||||
Db  301  EIHLHSLSPGPSK  313
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RESULT 10
US-10-705-757-2
; Sequence 2, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029910.52818US
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-705-757-2

```
Query Match            98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity  97.1%;  Pred. No. 4.7e-140;
Matches   304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:.|||.||||||||||||||||||||.|||||||.|||||||||||||||.||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313
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RESULT 11
US-10-377-268-9
; Sequence 9, Application US/10377268
; Publication No. US20040171062A1
;
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-377-268-9

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Query Match            98.1%;  Score 1636;  DB 4;  Length 313;
Best Local Similarity  97.1%;  Pred. No. 4.7e-140;
Matches   304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:.|||.||||||||||||||||||.|||||||.|||||||||||||||.||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313
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RESULT 12
US-10-951-389-18
; Sequence 18, Application US/10951389
; Publication No. US20050058627A1
;
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-951-389-18

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Query Match            98.1%;  Score 1636;  DB 5;  Length 313;
Best Local Similarity  97.1%;  Pred. No. 4.7e-140;
Matches   304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:.|||.||||||||||||||||||.|||||||.|||||||||||||||.||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313
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RESULT 13
US-10-951-406-18
; Sequence 18, Application US/10951406
; Publication No. US20050059630A1

GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-951-406-18

Query Match   98.1%; Score 1636; DB 5; Length 313;
Best Local Similarity   97.1%; Pred. No. 4.7e-140;
Matches 304;   Conservative   6; Mismatches   3; Indels   0; Gaps   0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSVSYSGIRVAD 60
        ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||:
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVSYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:::||:|||||||||||||||||:|||||||:|||||||||||||||||:||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
        |||||||||:|||
Db  301 EIHLHSLSPGPSK 313
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RESULT 14
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050639741A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-951-477-18

Query Match   98.1%; Score 1636; DB 5; Length 313;
Best Local Similarity   97.1%; Pred. No. 4.7e-140;
Matches 304;   Conservative   6; Mismatches   3; Indels   0; Gaps   0;

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Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGFGSVSYSGIRVAD 60
        ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||:
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVSYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||:::||:|||||||||||||||||:|||||||:|||||||||||||||||:||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
        |||||||||:|||
Db  301 EIHLHSLSPGPSK 313
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RESULT 15
US-10-977-087-18
; Sequence 18, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; TITLE OF INVENTION: AND THEIR METHODS OF USE V
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18

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;    LENGTH: 313
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-977-087-18

Query Match         98.1%;  Score 1636;  DB 5;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 4.7e-140;
Matches  304;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
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Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
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Qy  301 EIHLHSLSPSPSK 313
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Search completed: May  4, 2006, 05:32:06
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Biocceleration Ltd.
GenCore version 5.1.7

Run on: May 4, 2006, 05:27:44 ; Search time 15.3333 Seconds
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Title: US-10-705-757-4
Perfect score: 1668
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Scoring table: BLOSUM62
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Searched: 235405 seqs, 46284737 residues
Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA New:*
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12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1131.5	67.8	455	9	US-10-784-004-373	Sequence 373, Ap
2	869	52.1	334	8	US-10-511-937-2982	Sequence 2982, App
3	869	52.1	334	8	US-10-501-841-32	Sequence 32, Appl
4	866.5	51.9	311	9	US-10-501-841-40	Sequence 40, Appl
5	866.5	51.9	311	11	US-11-103-065-2	Sequence 2, Appli
6	381.5	22.9	256	8	US-10-105-928-690	Sequence 690, App
7	378.5	22.7	256	11	US-10-877-346-74	Sequence 74, App
8	367	22.0	504	11	US-11-087-099-9816	Sequence 9816, Ap
9	367	22.0	950	9	US-10-501-035-357	Sequence 357, App
10	364.5	21.9	631	11	US-11-241-056-11	Sequence 11, Appl
11	358	21.5	514	11	US-11-087-099-11500	Sequence 11500, A
12	355.5	21.3	256	9	US-10-877-346-72	Sequence 72, Appl
13	355.5	21.3	256	11	US-11-113-424-183	Sequence 183, App
14	350.5	21.0	504	11	US-11-087-099-12331	Sequence 12331, A
15	350	21.0	512	11	US-11-087-099-3997	Sequence 3997, Ap
16	350	21.0	514	11	US-11-087-099-3612	Sequence 3612, Ap
17	348	20.9	472	11	US-11-087-099-11838	Sequence 11838, A
18	346	20.7	86	9	US-10-501-841-37	Sequence 37, Appl
19	346	20.7	464	11	US-11-096-568A-22124	Sequence 22124, A
20	344	20.6	513	11	US-11-087-099-11726	Sequence 11726, A
21	342.5	20.5	722	9	US-10-784-004-435	Sequence 435, App
22	342.5	20.5	722	9	US-10-784-004-951	Sequence 951, App
23	340.5	20.4	651	9	US-10-770-726-67	Sequence 67, Appl
24	340.5	20.4	651	11	US-11-177-138-10	Sequence 10, Appl
25	338.5	20.3	619	11	US-11-087-099-12402	Sequence 12402, A
26	338	20.3	713	9	US-10-995-561-881	Sequence 881, Appl
27	338	20.3	729	9	US-10-995-561-878	Sequence 878, Appl
28	338	20.3	737	9	US-10-995-561-880	Sequence 880, App
29	338	20.3	744	9	US-10-995-561-876	Sequence 876, App
30	338	20.3	753	9	US-10-995-561-877	Sequence 877, App
31	336.5	20.2	445	11	US-11-096-568A-32575	Sequence 32575, A
32	335.5	20.1	689	9	US-10-204-639-17	Sequence 17, Appl
33	334.5	20.1	651	11	US-11-087-099-1886	Sequence 1886, Ap
34	333.5	20.0	715	9	US-10-204-639-65	Sequence 65, Appl
35	332	19.9	620	11	US-11-087-099-3898	Sequence 3898, Ap
36	331.5	19.9	658	9	US-10-979-095-6	Sequence 6, Appli
37	329.5	19.8	448	11	US-11-096-568A-18364	Sequence 18364, A
38	327	19.6	516	11	US-11-087-099-1845	Sequence 1845, Ap
39	325.5	19.5	439	11	US-11-096-568A-20431	Sequence 20431, A
40	325.5	19.5	443	11	US-11-096-568A-20430	Sequence 20430, A
41	325	19.5	277	11	US-11-151-601-4	Sequence 4, Appli
42	325	19.5	513	11	US-11-087-099-7631	Sequence 7631, Ap
43	323.5	19.4	611	11	US-11-087-099-8358	Sequence 8358, Ap
44	322.5	19.3	278	8	US-10-370-959-17	Sequence 17, Appl
45	322.5	19.3	278	8	US-10-370-959-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-784-004-373

; Sequence 373, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 373
; LENGTH: 455
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-373

Query Match   67.8%; Score 1131.5; DB 9; Length 455;
Best Local Similarity   72.5%; Pred. No. 3e-89;
Matches 214; Conservative   30; Mismatches   44; Indels   7; Gaps   5;

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Qy   58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERDPS 115
          :||:|||||| :|:| | :|| | |  |:||||||:||  ::|  ||||||||||: |
Db  189 IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFEREPDG 247

Qy  116 FVLILEREPPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
          |:|:|| |.||||||||||||||  | ||.||.|||.|||||||||| :||||||||:|:
Db  248 FLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 307

Qy  176 DLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
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Qy  236 VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
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Db  368 VCGDIPFEQDEETLRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 422
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RESULT 2

US-10-511-937-2982
; Sequence 2982, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50612000104
; CURRENT APPLICATION NUMBER: 5066120000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3317
; SOFTWARE: Patentin version 3.2

; SEQ ID NO 2982
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2982

Query Match 52.1%; Score 869; DB 8; Length 334;
Best Local Similarity 55.9%; Pred. No. 6.5e-67;
Matches 170; Conservative 43; Mismatches 73; Indels 18; Gaps 3;

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Qy  310 SPSK 313
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RESULT 3
US-10-501-841-32
; Sequence 32, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne

; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 32
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-32

Query Match 52.1%; Score 869; DB 9; Length 334;
Best Local Similarity 55.9%; Pred. No. 6.5e-67;
Matches 170; Conservative 43; Mismatches 73; Indels 18; Gaps 3;

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; Sequence 40, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-014402PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40

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;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-501-841-40

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Best Local Similarity    58.0%;  Pred. No. 9.7e-67;
Matches 166;  Conservative 41;  Mismatches 74;  Indels 5;  Gaps 2;

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Qy      88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPPVQDLFDFITERGALQEELAR 145
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Qy     146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVTDFDGTR 205
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Qy     266 LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP 311
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RESULT 5
US-11-103-065-2
;   Sequence 2, Application US/11103065
;   Publication No. US20050282189A1
;   GENERAL INFORMATION:
;   APPLICANT: Meyers, Rachel E., Lora, Jose M.
;   TITLE OF INVENTION: 2150, Human Protein Kinase Family
;       Member and Uses Therefor
;   FILE REFERENCE: MPI2001-137P1RNM
;   CURRENT APPLICATION NUMBER: US/11/103,065
;   CURRENT FILING DATE: 2005-04-11
;   PRIOR APPLICATION NUMBER: US/10/184,563
;   PRIOR FILING DATE: 2002-06-27
;   PRIOR APPLICATION NUMBER: 60/301,702
;   PRIOR FILING DATE: 2001-06-28
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 2
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-103-065-2

Query Match              51.9%;  Score 866.5;  DB 11;  Length 311;
Best Local Similarity    58.0%;  Pred. No. 9.7e-67;
Matches 166;  Conservative 41;  Mismatches 74;  Indels 5;  Gaps 2;

Qy      28 GKEKEPLESQYQVGPLLGSGGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
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Db      22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPNRVLGWSPLSDSVTCP 81

Qy      88 MEVVLLKKVSS--GFSGVIRLLDWFERPDSFVLILERPPVQDLFDFITERGALQEELAR 145
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Db      82 LEVALLWKVGAGGHPGVIRLLDWFETQEEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy     146 SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVTDFDGTR 205
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Db     202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHPPAHVSPDCCA 261

Qy     266 LIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATAEIHLHSLSPSP 311
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Db     262 LIRRCLAPKPSSRPSLEEILLDPWMQ---TPAEDVPLNPSKGGPAP 304
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RESULT 6
US-10-505-928-690
;   Sequence 690, Application US/10505928
;   Publication No. US20060085332A1
;   GENERAL INFORMATION:
;   APPLICANT: Ludwig Institute for Cancer Research et al.
;   TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;   FILE REFERENCE: 28967/39178
;   CURRENT APPLICATION NUMBER: US/10/505,928
;   CURRENT FILING DATE: 2004-08-27
;   PRIOR APPLICATION NUMBER: US 60/363,019
;   PRIOR FILING DATE: 2002-03-07
;   NUMBER OF SEQ ID NOS: 866
;   SOFTWARE: Patentin 3.2
;   SEQ ID NO 690
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-690

Query Match              22.9%;  Score 381.5;  DB 8;  Length 661;
Best Local Similarity    34.8%;  Pred. No. 9e-25;
Matches 93;  Conservative 47;  Mismatches 112;  Indels 15;  Gaps 8;

Qy      31 KEPLESQYQVGPLLGSGGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV 90
           |  |  |   | |||  | |||    | |   | || |||    | |   |    |: |
Db      48 KHNLKHRYELQETLGKGTYGKVKRATERFSGRVAIKSIRKDKIKDEQDM---VHIRREI 104

Qy      91 VLLKKVSSGFSGVIRLLDWFERPDSFVLILERPPVQDLFDFITERGALQEELARSFFWQ 150
           ||  |:    |||||||||||  |||| | |   |   | |   |   |:|:    :|||
Db     105 EIMS--SLNHPHIISIYEVENKDKIVIIMEYASK-GELYDYISERRRLSERETHHFFRQ 161

Qy     151 VLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVTDFDGTRVYSP 209
           ::|||||||||||||||||||||||  |||| | ||||| ||    |:   |  :| |
Db     162 IVSAVHYCHKNGVVHRDIKLENILLDDN-CNIKIADFGLSNLYQKDKFLQTFCGSPLYAS 220

Qy     210 PEWIRYHRYHGRSAAVWSLGILLYDMVCGDIP---FEHD---EEIVKGQVYFRQRVSSEC 263
           |  ||   |  |  :|  | :|  |  | |:|   |:|    :|  |    |||| | |
Db     221 PEIVNGRPYRGPEVDSWALGVLLYTLVCGTMPFDGDHKNLIRQISSGE-YREPTQPSDA 279

Qy     264 QHLIRWCLSLRPSDRPSFEEIQNHPWM 290
           |||||||||||||||||||||||||||
Db     280 RGLIRWMLMVNPDRRATIEDIANHWWV 306
```

```
RESULT 7
US-10-877-346-74
;   Sequence 74, Application US/10877346
;   Publication No. US20060014153A1
;   GENERAL INFORMATION:
;   APPLICANT: Gerlach, Valerie L
;   APPLICANT: MacDougall, John R
;   APPLICANT: Smithson, Glennda
;   APPLICANT: Millet, Isabelle
;   APPLICANT: Stone, David
;   APPLICANT: Gunther, Erik
;   APPLICANT: Ellerman, Karen
;   APPLICANT: Grosse, William M
;   APPLICANT: Alsobrook II, John P
;   APPLICANT: Lepley, Denise M
;   APPLICANT: Burgess, Catherine E
;   APPLICANT: Padigaru, Muralidhara
;   APPLICANT: Kekuda, Ramesh
;   APPLICANT: Spytek, Kimberly A
;   APPLICANT: Leach, Martin D
;   APPLICANT: Shimkets, Richard A
;   TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
;   FILE REFERENCE: 21402-124
```

; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

Query Match   22.7%; Score 378.5; DB 9; Length 256;
Best Local Similarity 36.2%; Pred. No. 5e-25;
Matches 96; Conservative 49; Mismatches 97; Indels 23; Gaps 9;

Qy 38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
      |:|| ||||||:: :||| |:| | || ||:: ||:: ||:|
Db   1 YELGEKLGSGAFGKVYKGHKDTGEIVAIKILKKRSLSE----KKKKFLREIQILRRLS 55

Qy 98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERG-ALQEELARSFFWQVLEAVR 156
      :|||| ||| | :| | ||:| :|:|
Db 56 --HPNIVRLLGVFEEDHLYLVMEYMEG--GDLFDYLRRNGLLLSEKEAKKIALLQILRGIE 112

Qy 157 HCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVY----TDFDGTRVYSPPEWI 213
      |:||| |||||| |||| |||:||| |:| ||||| |
Db 113 YLHSRGIVHRDLKPENILLDEN--GTVKIADFGLARKLESSSSYEKLTTFVGTPEYMAPEVL 171

Qy 214 RYRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEIVKGQVYFRQRV------SSECQ 264
       |||| |:|||||| |: || |: | ||
Db 172 EGRGYSSK-VDVWSLGVILYELLTGKLPPGIDPLEELFRIKERPRLRLPLPPNCSEELK 230

Qy 265 HLIRWCLSLRPSDRPSFEEIQNHPW 289
       :||| ||: ||| ||||
Db 231 DLIKKCLNKDPEKRPTAKEILNHPW 255

;
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match   22.0%; Score 367; DB 11; Length 504;
Best Local Similarity 34.4%; Pred. No. 1.1e-23;
Matches 90; Conservative 51; Mismatches 105; Indels 16; Gaps 8;

Qy 38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
      :|| ||||||:: :| | ||:| :|:
Db   8 YKLGKTLGTGSFGKVKIAEHALTGHKVAIKILNRRKIQN---LDMEEKVRREIKILRLFM 64

Qy 98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
      |:| || | | :| || |:|||
Db 65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 121

Qy 158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
      ||||| |||||| ||||||||:|| |:| |||||:|
Db 122 CHRNMVVHRDLKPENLLLD--SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy 217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI-------VKGQVY-FRQRVSSECQHLIRW 269
       || |||| || |||| :| |: |
Db 181 LYAGPEVDVDWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy 270 CLSLRPSDRPSFEEIQNHPWMQ 291
       || |||| ||||
Db 240 MLVVDPMKRITIPEIRQHPWFQ 261

RESULT 8
US-11-087-099-9816
; Sequence 9816, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT

RESULT 9
US-10-501-035-357
; Sequence 357, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 357
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-357

Query Match   22.0%; Score 367; DB 9; Length 950;
Best Local Similarity 31.8%; Pred. No. 2.5e-23;
Matches 87; Conservative 52; Mismatches 113; Indels 22; Gaps 7;

Qy 38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
      :|| ||||||:: :| | || : |:
Db 44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL---DAVNLEKIYREVQIMKMLD 99

Qy 98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
      |:| | || | :| :|
Db 100 --HPHIIKLYQVMETKSMLYLVTEYAKQ-GEIFDYLANHGRLNESEARRKFWQLLSAVDY 156

Qy 158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
      ||| |||| | || |||||||||:|| |:||||||:|
Db 157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ 215

Qy 217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD-------EEIVKGQVYFRQRVSSECQHLIRWC 270
       ||| ||: ||| || ||: ||: |||
Db 216 QYEGPQLDIWSMGVVLYVLLCGALPFDGPTLPILRQRVLEGRFRIPYFMSEDCEHLIRRM 275

Qy 271 LSLRPSDRPSFEEIQNHPWM--------QDVLLPQ 297
       |||| |||| |||
Db 276 LVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQ 309

RESULT 10
US-11-241-056-11
Sequence 11, Application US/11241056
Publication No. US20060024807A1
GENERAL INFORMATION:
  APPLICANT: Immunex Corporation
  APPLICANT: Bird, Timothy A.
  APPLICANT: Virca, G. Duke
  APPLICANT: Martin, Unja
  APPLICANT: Anderson, Dirk M.
  TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
  FILE REFERENCE: 2923-US
  CURRENT APPLICATION NUMBER: US/11/241,056
  CURRENT FILING DATE: 2005-09-30
  PRIOR APPLICATION NUMBER: US/09/980,464
  PRIOR FILING DATE: 2001-11-27
  NUMBER OF SEQ ID NOS: 36
  SOFTWARE: Patentin version 3.1

SEQ ID NO 11
  LENGTH: 631
  TYPE: PRT
  ORGANISM: Mus musculus

Query Match   21.9%; Score 364.5; DB 11; Length 631;
Best Local Similarity 32.9%; Pred. No. 2.4e-23;
Matches   96; Conservative 49; Mismatches 116; Indels 31; Gaps 9;

Qy   22 ANKLAPGKEKEP--------------------------------LESQYQVGPLLGSGGFGSVYSGIRVADNLPV 64
                                                            :|| |: ||:|||||||||:|:|:
Db   24 ARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKA-RESSGRLV 82

Qy   65 AIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLILERPE 124
                |:|::||||| |:| ||:|::||| ||: ||||:||||||: :||||
Db   83 AIKSIRKDKIKDEQDL---LHIRREIEIMS--SLNHPHIIAIHEVFENSSKIVIMEYAS 137

Qy   125 PVQDLFDITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILLIDLNRGELKL 184
                || |:|:| || |:||:| | ||:|||: |:: ||:|||||||||||| ::|:| |::|
Db   138 R-GDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDAN-GNIKI 195

Qy   185 IDFG-GGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFE 243
                |||| || |||:|||:|||||||||||||:|||:| ||: ||||||||||:|:|||||||
Db   196 ADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILLVHGTMPFD 255

Qy   244 -HDEEIVKGQV-----YFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
                 |:|:||| |: |||:|:|||||||||||||:|||||||||||||:|||
Db   256 GQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASHWWV 307

Qy   270 CLSLRPSDRPSFEEIQNHPWMQ 291
               |||||||||||||||||||:| |
Db   251 MLIVDPMKRMTIPSIRLHPWFQ 272

RESULT 11
US-11-087-099-11500
Sequence 11500, Application US/11087099
Publication No. US20060419611A1
GENERAL INFORMATION:
  APPLICANT: Abad, Mark S. et al.
  TITLE OF INVENTION: Genes and Uses for Plant Improvement
  FILE REFERENCE: 38-21(53450)B EP
  CURRENT APPLICATION NUMBER: US/11/087,099
  CURRENT FILING DATE: 2005-03-22
  NUMBER OF SEQ ID NOS: 12464

SEQ ID NO 11500
  LENGTH: 514
  TYPE: PRT
  ORGANISM: Lycopersicon esculentum

Query Match   21.5%; Score 358; DB 11; Length 514;
Best Local Similarity 33.2%; Pred. Mismatches 105; Indels 16; Gaps 8;
Matches   87; Conservative 54;

Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97

RESULT 12
US-10-877-346-72
Sequence 72, Application US/10877346
Publication No. US20060141532A1
GENERAL INFORMATION:
  APPLICANT: Gerlach, Valerie L
  APPLICANT: MacDougall, John R
  APPLICANT: Smithson, Glennda
  APPLICANT: Millet, Isabelle
  APPLICANT: Stone, David
  APPLICANT: Gunther, Erik
  APPLICANT: Ellerman, Karen
  APPLICANT: Grosse, William M
  APPLICANT: Alsobrook II, John P
  APPLICANT: Lepley, Denise M
  APPLICANT: Burgess, Catherine E
  APPLICANT: Padigaru, Muralidhara
  APPLICANT: Kekuda, Ramesh
  APPLICANT: Spytek, Kimberly A
  APPLICANT: Leach, Martin D
  APPLICANT: Shimkets, Richard A
  TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
  FILE REFERENCE: 21402-124
  CURRENT APPLICATION NUMBER: US/10/877,346
  CURRENT FILING DATE: 2004-06-25
  PRIOR APPLICATION NUMBER: US/09/964,956
  PRIOR FILING DATE: 2001-09-26
  PRIOR APPLICATION NUMBER: 60/235,631
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: 60/235,633
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: 60/235,808
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: 60/236,064
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: 60/236,065
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: 60/236,066
  PRIOR FILING DATE: 2000-09-27
  PRIOR APPLICATION NUMBER: 60/236,135
  PRIOR FILING DATE: 2000-09-28
  PRIOR APPLICATION NUMBER: 60/237,434
  PRIOR FILING DATE: 2000-10-03
  PRIOR APPLICATION NUMBER: 60/238,321
  PRIOR FILING DATE: 2000-10-05
  Remaining Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 127
  SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 72
  LENGTH: 256
  TYPE: PRT
  ORGANISM: Artificial Sequence
  FEATURE:

Db   19 YKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM 75

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
                :|:| ||| |:||:| || :|| : :| :| |:|||:||||:| | | ||||| | :|
Db   76 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY 132

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIIDFGSGALLKDTVTDFD-GTRVYSPPEWIRYH 216
                |:| |||||||||||| ||||:|||| ||||:| ||||:|||:| |||||||||||:|:
Db   133 CHRNMVVHRDLKFENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 191

Qy   217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSECQHLIRW 269
                ||:|:|| | ||| || ||: | |:||: : :| ||||:| |::|:||| |: |
Db   192 LYAGPEVDVDWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR 250

Qy   270 CLSLRPSDRPSFEEIQNHPWMQ 291
                |||||||||||||||||||:| |
Db   251 MLIVDPMKRMTIPSIRLHPWFQ 272

; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/Threonine protein kinase Consensus
; OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match   21.3%;   Score 355.5; DB 9; Length 256;
Best Local Similarity   33.0%; Pred. No. 4.7e-23;
Matches 88; Conservative 56; Mismatches 96; Indels 27; Gaps 8;

Qy   38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
           :||.|:||||||||.:||.|||.::|:   :.||||||.:|:||.:||||:
Db   1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL----KKKKRERILREIKILKKLD 56

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db   57 --HPNIVKLYDVFEDDKLYLVWEYCEG-GDLFDLLKRRGRLSEDEARFYARQILSALEY 113

Qy 158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY 215
Db 114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy 216 HRYHGRSAAVWSLGILLLYDMVCGDIPEHDEIIVKGQVYFRQ-----------RVSSE 262
Db 172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPPPEWKISPE 228

Qy 263 CQHLIRWCLSLRPSDRPSFEEIQNHPW 289
Db 229 AKDLIKLLLVKDPEKRLTAEEALEHPF 255

RESULT 13
US-11-424-183
Sequence 183, Application US/11113424
; Publication No. US2005026071A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 183
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-11-113-424-183

Query Match   21.3%;   Score 355.5; DB 11; Length 256;
Best Local Similarity   33.0%; Pred. No. 4.7e-23;
Matches 88; Conservative 56; Mismatches 96; Indels 27; Gaps 8;

Qy   38 YQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
Db   1 YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL----KKKKRERILREIKILKKLD 56

Qy   98 SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db   57 --HPNIVKLYDVFEDDKLYLVWEYCEG-GDLFDLLKRRGRLSEDEARFYARQILSALEY 113

Qy 158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKD--TVYTDFDGTRVYSPPEWIRY 215
Db 114 LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL 171

Qy 216 HRYHGRSAAVWSLGILLLYDMVCGDIPEHDEIIVKGQVYFRQ-----------RVSSE 262
Db 172 GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPPPEWKISPE 228

Qy 263 CQHLIRWCLSLRPSDRPSFEEIQNHPW 289
Db 229 AKDLIKLLLVKDPEKRLTAEEALEHPF 255

RESULT 14
US-11-087-099-12331
Sequence 12331, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12331
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-12331

Query Match   21.0%;   Score 350.5; DB 11; Length 504;
Best Local Similarity   32.5%; Pred. No. 2.9e-22;
Matches 98; Conservative 53; Mismatches 112; Indels 39; Gaps 12;

Qy   28 GKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVADNL----PVAIKHVEKDRISDWGELPNG 83
Db   7 GIAESPYLRNYRVGKTLGHGSFGKV------------------------------------ 53

Qy   84 TRVP-MEVVLLKKVS----SGFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGA 138
Db   54 -KTPDMEEKLRREIKICRLFVHPHVIRLYEVIETPTDIYVVMEYVKS-GELFDYIVEKGR 111

Qy 139 LQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVY 198
Db 112 LQEDEARKIFQQIIAGVEYCHKNQMVVHRDLKPENLLLDARR-NVKIADFGLGNIMRDGHF 170

Qy 199 TDFD-GTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPEHDEI-----VKG 251
Db 171 LKTSCGSPNYAAPEVVSGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKS 229

Qy 252 QVY-FRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVL-----LPQATAEIHLH 305
Db 230 GVYTLPSHLSPLARDLIPRMLIVDPMKRISVPDIRQHQWFKIHLPRYLAVPPPDARQHLK 289

Qy 306 SL 307
Db 290 KL 291

RESULT 15
US-11-087-099-3997
Sequence 3997, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.

```
;
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3997
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-3997

Query Match     21.0%;  Score 350;  DB 11;  Length 512;
Best Local Similarity   31.7%;  Pred. No. 3.3e-22;
Matches   84;  Conservative   60;  Mismatches   99;  Indels   22;  Gaps    8;

Qy       38 YQVGPLLGSSGGFGSSVYSGIRVADNL------PVAIKHVEKDRISDWGELPNGTRVPMEVVLL   93
              :||:       |:::||       |:|:       |||||||||||||||||||||||||
Db       19 YKLGKTLGIGSFGKV----KIAEHTLIGHKVAVKILNRRKIRN---MDMEEKVSREIKIL   71

Qy       94 KKVSSGFSGVIRLLDWFERPDSFVLILERPEPVQDLFPDFITERGALQEELARSFFWQVLE   153
              :||::  | ||||||||||||||   ::|:|  |||:|||||||||||||||::
Db       72 RLFMHGH--ISRLYEVIETPSDIYVVMEYVKS-GELFDYIVERKGRLQEDEARNFFQQIIS   128

Qy      154 AVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEW   212
              ||| |  :|||||||||||  :|| ||  |: ||| || |   |:| ||
Db      129 GVEYCHINMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEV   187

Qy      213 IRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIVKGQYYFRQRVSSECQHL   266
              ||||:   || |||:|||||||| : |:|:|| ||     || |||:|||:||:| ||
Db      188 ISGKLYAGPEVDVWSCGVILYALLCGTLPFDDENIPNLFKKIKGGYITLPSHLSAGARDL   247

Qy      267 IRWCLSLRPSDRPSFEEIQNHPWMQ   291
              || ||  ||:|||||:|| |||||
Db      248 IPRMLIVDPMKRMTIPEIRLHPWFQ   272

Search completed: May  4, 2006,  05:32:58
Job time : 16.3333 secs
```

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OM protein - protein search, using sw model

GenCore version 5.1.7
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Run on: May 4, 2006, 05:12:40 ; Search time 113.667 Seconds
(without alignments)
1209.902 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRAAPCNDL..........LLPQATAEIHLHSLSPPSK 313
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1908:*
2: geneseqp1990s:*
3: geneseqp2008:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	5	ABG33016	Abg33016 Rat prote
2	1668	100.0	313	6	AAO19789	Aao19789 Rat PIM1
3	1668	100.0	313	6	ABR62938	Abr62938 Rat serin
4	1668	100.0	313	9	AEB96039	Aeb96039 Norway ra
5	1636	98.1	313	5	ABP54943	Abp54943 Human pim
6	1636	98.1	313	5	ABG33017	Abg33017 Human pro
7	1636	98.1	313	6	AAO19788	Aao19788 Human PIM
8	1636	98.1	313	7	ABU61613	Abu61613 Human PIM
9	1636	98.1	313	7	ABR62939	Abr62939 Human ser
10	1636	98.1	313	7	ADE55368	Ade55368 Human Pro
11	1636	98.1	313	7	ADF45083	Adf45083 Human kin
12	1636	98.1	313	8	ADO19690	Ado19690 Human PRO
13	1636	98.1	313	8	ADR88370	Adr88370 Human PIM
14	1636	98.1	313	8	ADP24227	Adp24227 PRO polyp
15	1636	98.1	313	9	ADT07365	Adt07365 Human pro
16	1636	98.1	313	9	ADT14636	Adt14636 Human Pim
17	1636	98.1	313	9	ADY86782	Ady86782 Human pim
18	1636	98.1	313	9	AEA89424	Aea89424 Human Pim
19	1636	98.1	313	9	AEB96037	Aeb96037 Human PIM
20	1623	97.3	313	2	AAW08139	Aaw08139 Human cyt
21	1623	97.3	313	5	AAY87959	Aay87959 Human CR7
22	1623	97.3	313	8	ADI57202	Adi57202 Human PIM
23	1623	97.3	313	8	ADN03170	Adn03170 Human PIM
24	1623	97.3	313	9	ADY85580	Ady85580 Catalytic

ALIGNMENTS

RESULT 1
ID ABG33016
AC ABG33016;
XX
DT 20-DEC-2002 (first entry)
XX
DE Rat protein kinase phosphorylation site #2.
XX
KW HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW Waldenstrom's macroglobulinaemia; WM; rat.
XX
OS Rattus norvegicus.
XX
PN US2002115120-A1.
XX
PD 22-AUG-2002.
XX
PF 04-OCT-2001; 2001US-00971791.
XX
PR 26-JAN-1999; 99US-00237543.
PR 23-AUG-2000; 2000US-00644450.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
DR WPI; 2002-712471/77.
XX
PT Modulating levels or activity of HKID-1 polypeptides, a member of
PT serine/threonine kinase superfamily, for treating cancer, by contacting
PT cell expressing the polypeptide with a modulator of the polypeptide.
XX
PS Example 3; Page 39-40; 48pp; English.
XX
CC The invention describes a method of modulating the level or activity of
CC human HKID-1 polypeptide, a member of serine/threonine kinase
CC superfamily. The method involves contacting a cell expressing the
CC polypeptide or nucleic acid with an agent to modulate the level or
CC activity of polypeptide, or level of nucleic acid molecule. The method is
CC useful for modulating the level or activity of HKID-1 polypeptide or
CC polynucleotide in a subject having or predisposed to having a disorder
CC involving cancer. Modulating HKID-1 expression or activity is useful for
CC therapeutic purposes, for treating cellular proliferative and/or

25	1584	95.0	313	5	ABG33015	Abg33015 Mouse pro
26	1584	95.0	313	6	AAO19790	Aao19790 Murine PI
27	1584	95.0	313	7	ABR62940	Abr62940 Mouse ser
28	1584	95.0	313	8	ADN97347	Adn97347 Murine Pi
29	1584	95.0	313	9	ADR88371	Adr88371 Mus muscu
30	1584	95.0	313	9	AEA19261	Aea19261 Mouse Pim
31	1578	94.6	313	6	AEB96041	Aeb96041 House mou
32	1345	80.6	253	8	AEA19263	Aea19263 Mouse Pim
33	1304.5	80.6	257	2	ADI57241	Adi57241 PIM1 domi
34	1267.5	78.2	254	2	AAY43942	Aay43942 Rat domai
35	1229	76.0	257	2	ADK71853	Adk71853 Human kin
36	1137	68.2	233	8	ADT07367	Adt07367 Human pro
37	1137	68.2	323	8	ADR88376	Adr88376 Columnix
38	1137	68.2	374	8	AAY06886	Aay06886 HWHHJ20 p
39	1135	68.2	374	4	ADX91611	Adx91611 Plant ful
40	1135	68.0	326	4	AAB29788	Aab29788 Human ser
41	1135	68.0	326	5	AAE23834	Aae23834 Human HKI
42	1135	68.0	326	5	ABG33011	Abg33011 Human ser
43	1135	68.0	326	7	ABR62932	Abr62932 Human cal
44	1135	68.0	326	8	ADJ96625	Adj96625 Human pro
45	1135	68.0	326	8	ADI97960	Adi97960 Human PIM

CC differentiation disorders including cancer or haematopoietic neoplastic
CC disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC leukaemia (CML) and Waldenström's macroglobulinaemia (WM). This is the
CC amino acid sequence of a rat protein kinase phosphorylation site
XX
SQ Sequence 313 AA;

Query Match   100.0%;   Score 1668; DB 5; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Pred. No. 9.6e-159; Indels   0; Gaps   0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
        |||||||||||||
Db  301 EIHLHSLSPSPSK 313
```

RESULT 2
ID AAO19789 standard; protein; 313 AA.
XX
AC AAO19789;
XX
DT 11-AUG-2003 (first entry)
XX
DE Rat PIM1 kinase.
XX
KW Rat; PIM1 kinase; PIM3 kinase; pain; analgesic.
OS Rattus sp.
XX
PN WO2002093173-A2.
XX
PD 21-NOV-2002.
XX
PF 13-MAY-2002; 2002WO-EP005234.
PR 11-MAY-2001; 2001DE-0102305S.
XX
PA (CHEP) GRUENENTHAL GMBH.
XX
PI Weihe E, Schaefer MK;
XX
DR WPI; 2003-120715/11.
DR N-PSDB; AB269187.
XX
PT Method for identifying analgesics, useful particularly for treating
PT chronic pain, by screening compounds for interaction with PIM-1 or -3
PT kinase, or related compounds.
XX
PS Claim 1; Fig 1D; 97pp; German.
XX
CC The present invention relates to a method of identifying pain-regulating
CC compounds, involving screening candidate compounds for interaction with

---

CC PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC useful for treating chronic pain, particularly of neuropathic or
CC inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC neurodegenerative diseases). The present sequence is rat PIM1 kinase
XX
SQ Sequence 313 AA;

Query Match   100.0%;   Score 1668; DB 6; Length 313;
Best Local Similarity   100.0%;
Matches 313; Conservative   0; Mismatches   0; Pred. No. 9.6e-159; Indels   0; Gaps   0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy  301 EIHLHSLSPSPSK 313
        |||||||||||||
Db  301 EIHLHSLSPSPSK 313
```

RESULT 3
ID ABR62938 standard; protein; 313 AA.
XX
AC ABR62938;
XX
DT 04-DEC-2003 (first entry)
XX
DE Rat serine/threonine protein kinase PIM-1.
XX
KW Rat; PIM-1; protein kinase; enzyme.
OS Rattus norvegicus.
XX
PN WO2003060130-A2.
XX
PD 24-JUL-2003.
XX
PF 20-JAN-2003; 2003WO-EP000492.
PR 19-JAN-2002; 2002EP-00001401.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Korn M, Mueller G, Schneider R, Tschank G;
XX
DR WPI; 2003-598536/56.
XX
PT New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT treating insulin resistance or type 2 diabetes mellitus.
XX
PS Example 2; Page 39; 40pp; English.
XX
CC The present sequence is the protein sequence of the rat serine/threonine
CC protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
CC paralogues of novel human and murine PIM-3 proteins (see ABR62932 and

CC   ABR62933) of the invention, which are therefore expected to be involved
CC   in cancer and cell growth regulation. PIM-3 is also involved in the
CC   development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
XX
SQ   Sequence 313 AA;

Query Match   100.0%;   Score 1668;   DB 7;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 9.6e-159;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPSPSK 313
       |||||||||||||
Db   301 EIHLHSLSPSPSK 313

RESULT 4
AEB96039
ID   AEB96039 standard; protein; 313 AA.
XX
AC   AEB96039;
XX
DT   20-OCT-2005   (first entry)
XX
DE   Norway rat PIM-1 serine-threonine kinase protein.
XX
OS   Rattus norvegicus.
XX
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
XX
PN   DE102004004894-A1.
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96038.
DR   REFSEQ; NP_058730.

XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
PT   similar use of PIM proteins or nucleic acids.
XX
PS   Claim 1; Fig 1D; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the Norway rat PIM-1 serine-
CC   threonine kinase protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match   100.0%;   Score 1668;   DB 9;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 9.6e-159;
Matches 313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPSPSK 313
       |||||||||||||
Db   301 EIHLHSLSPSPSK 313

RESULT 5
ABP54943
ID   ABP54943 standard; protein; 313 AA.
XX
AC   ABP54943;
XX
DT   13-JAN-2003   (first entry)
XX
DE   Human Pim1.
XX
KW   Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW   mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW   human; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200268444-A1.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005278.

PR 21-FEB-2001; 2001US-0271254P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
DR WPI; 2002-698650/75.
DR N-PSDB; ABV73989.
XX
PS Disclosure; Page 80-81; 113pp; English.
XX
PT Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,
PT prostate and ovarian cancer.
XX
CC The present sequence is the protein sequence of human Pim1, a protein
CC related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC polynucleotides and polypeptides of the invention encompass
CC polynucleotides and polypeptides having sequence similarity or sequence
CC identity to human TTK and other genes and gene products related to TTK,
CC such as Pim1. The invention is based on the finding that TTK is
CC differentially expressed in various forms of cancer. It provides methods
CC for the identification of cancerous cells, especially breast cancer and
CC colon cancer cells, by detection of expression levels of TTK, as well as
CC diagnostic, prognostic and therapeutic methods. These methods can be used
CC as the basis of rational therapy. Assays for identifying molecules that
CC modulate the activity of these genes in cancers, as well as methods of
CC inhibiting tumour growth by inhibiting the activity of TTK are also
CC provided
XX
SQ Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 5; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||| |||||||||||||||||||||||||||||||| |:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGCKEKEPLESQXQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
         |||||||| :||:|||||||||||||||||| :|||||||| ||||||||| |||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
         |||||||| ||||
Db 301 EIHLHSLSPGPSK 313

RESULT 6
ABG33017
ID ABG33017 standard; protein; 313 AA.
XX
AC ABG33017;
XX
DT 20-DEC-2002 (first entry)
XX
DE Human protein kinase phosphorylation site.
XX
KW HKID-1; serine/threonine kinase; cellular proliferative disorder;

KW differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW Waldenstrom's macroglobulinaemia; WM; human.
XX
OS Homo sapiens.
XX
PN US2002115120-A1.
XX
PD 22-AUG-2002.
XX
PF 04-OCT-2001; 2001US-00971791.
XX
PR 26-JAN-1999; 99US-00237543.
PR 23-AUG-2000; 2000US-00644450.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
PT Modulating levels or activity of HKID-1 polypeptides, a member of
PT serine/threonine kinase superfamily, for treating cancer, by contacting
PT cell expressing the polypeptide with a modulator of the polypeptide.
XX
PS Example 3; Page 40-41; 48pp; English.
XX
CC The invention describes a method of modulating the level or activity of
CC human HKID-1 polypeptide, a member of serine/threonine kinase
CC superfamily. The method involves contacting a cell expressing the
CC polypeptide or nucleic acid with an agent to modulate the level or
CC activity of polypeptide, or level of nucleic acid molecule. The method is
CC useful for modulating the level or activity of HKID-1 polypeptide or
CC polynucleotide in a subject having or predisposed to having a disorder
CC involving cancer. Modulating HKID-1 expression or activity is useful for
CC therapeutic purposes, for treating cellular proliferative and/or
CC differentiative disorders including cancer or haematopoietic neoplastic
CC disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC amino acid sequence of a human protein kinase phosphorylation site
XX
SQ Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 5; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||| |||||||||||||||||||||||||||||||| |:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGCKEKEPLESQXQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
         |||||||| :||:|||||||||||||||||| :|||||||| ||||||||| |||||||||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy 301 EIHLHSLSPSPSK 313
         |||||||| ||||
Db 301 EIHLHSLSPGPSK 313

RESULT 7

RESULT 8

```
ID   AAO19788 standard; protein; 313 AA.
XX
AC   AAO19788;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
OS   Homo sapiens.
XX
PN   WO20029173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-0102305.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   N-PSDB; AB269186.
DR   WPI; 2003-120715/11.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
SQ   Sequence 313 AA;
```

Query Match   98.1%; Score 1636; DB 6; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

```
Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYOVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYOVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
         ||||||| ||| ||||||||||||||||||||:|||||||:|||||||||||||||| ||
Db  241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
         |||||||||:|||
Db  301 EIHLHSLSPGPSK 313
```

```
ID   ABU61613 standard; protein; 313 AA.
XX
AC   ABU61613;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human PIM1 protein.
XX
KW   Human; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW   mitotic checkpoint gene; PIM1.
OS   Homo sapiens.
XX
PN   US2003045491-A1.
XX
PD   06-MAR-2003.
XX
PF   21-FEB-2002; 2002US-00081119.
XX
PR   23-FEB-2001; 2001US-0289813P.
XX
PA   (REIN/) REINHARD C.
PA   (JEFF/) JEFFERSON A B.
PA   (CHAN/) CHAN V W.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
DR   N-PSDB; ACA62265.
DR   WPI; 2003-456566/43.
XX
PT   Disclosure; Page 34-35; 79pp; English.
XX
CC   The invention relates to detecting cancer (other than ovarian cancer) in
CC   a subject, comprising comparing the expression levels of tyrosine
CC   threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
CC   polynucleotide in a test cell obtained from the subject and in a normal
CC   non-cancer cell, where an increase in the expression level of TTK protein
CC   or nucleic acid in the test cell compared to that in the normal cell,
CC   indicates the presence of cancer other than ovarian cancer. Also included
CC   are reducing growth of a cancerous cell (by contacting a cancerous cell
CC   with an amount of an agent effective to reduce TTK polypeptide activity
CC   in the cell), an assay for identifying a candidate agent that reduces
CC   growth of a cancerous cell (comprising: (i) detecting the activity of a
CC   TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC   the activity of TTK polypeptide in the presence of a candidate
CC   relative to TTK polypeptide activity in the absence of the candidate
CC   agent), identifying an agent that reduces TTK activity (comprising: (i)
CC   contacting a cancerous cell displaying elevated expression of a TTK-
CC   encoding polynucleotide with a candidate agent; and (ii) determining the
CC   effect of the candidate agent on TTK polypeptide activity) and assessing
CC   the prognosis of a cancerous disease other than ovarian cancer in a
CC   subject (comprising: (i) detecting expression of TTK -encoding
CC   polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC   level of expression of TTK-encoding polynucleotide in the test cancer
CC   cell with a level of expression of the polynucleotide in a control non-
CC   cancer cell, where the level of expression of TTK in the test cancer cell
CC   relative to the level of expression in the control non-cancer cell is
CC   indicative of the prognosis of the cancerous disease). The methods are
CC   useful for detecting cancer (other than ovarian cancer) in a subject,
CC   reducing growth of cancerous cells, identifying a candidate agent that
CC   reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC   activity and assessing the prognosis of a cancerous disease other than
CC   ovarian cancer. The methods are also useful for determining the ability
CC   of a subject to respond to a particular therapy e.g. as a basis of
CC   rational therapy. The present sequence represents a closely related
CC   protein to human TTK, in this case human PIM1 (not defined)
XX
```

```
SQ   Sequence 313 AA;

Qy   Query Match    98.1%;  Score 1636;  DB 7;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 1.6e-155;
Matches 304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          ||||||| ::|||:|||||||||||||||||||:|||||||:|||||||| |||||||:||
Db    241 PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLAIRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy    301 EIHLHSLSPSPSK 313
          |||||||| |||
Db    301 EIHLHSLSPGPSK 313


RESULT 9
ABR62939
ID   ABR62939 standard; protein; 313 AA.
XX
AC   ABR62939;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human serine/threonine protein kinase PIM-1.
XX
KW   Human; PIM-1; protein kinase; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2003060130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-0000141.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 40; 40pp; English.
XX
CC   The present sequence is the protein sequence of the human
CC   serine/threonine protein kinase and proto-oncogene, PIM-1.  PIM-1 proteins
CC   are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC   and ABR62931) of the invention, which are therefore expected to be
CC   involved in cancer and cell growth regulation.  PIM-3 is also involved in
CC   the development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
XX
SQ   Sequence 313 AA;

Qy   Query Match    98.1%;  Score 1636;  DB 7;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 1.6e-155;
Matches 304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERREPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          ||||||| ::|||:|||||||||||||||||||:|||||||:|||||||| |||||||:||
Db    241 PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLAIRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy    301 EIHLHSLSPSPSK 313
          |||||||| |||
Db    301 EIHLHSLSPGPSK 313


RESULT 10
ADE55368
ID   ADE55368 standard; protein; 313 AA.
XX
AC   ADE55368;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein AAA60089, SEQ ID NO 1183.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333147P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C, D'urso D, Befort K, Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAA60089.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
```

PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying the novel polynucleotide
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic construction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 7; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||:.|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
         ||||||| .:|||.:||||||||||||||||.||||||.||||||||||||||||.:||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
         |||||||||||||
Db 301 EIHLHSLSPGPSK 313

RESULT 11
XX
ID ADF45083 standard; protein; 313 AA.
XX
AC ADF45083;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase PIM1.
XX

KW Human; protein kinase; enzyme; inhibitor; PIM1.
XX
OS Homo sapiens.
XX
PN WO200308121O-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
PT Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 52; 260pp; English.
XX
CC The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 7; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||:.|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
         ||||||| .:|||.:||||||||||||||||.||||||.||||||||||||||||.:||
Db 241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
         |||||||||||||
Db 301 EIHLHSLSPGPSK 313

RESULT 12
XX
ID ADO19690 standard; protein; 313 AA.
XX
AC ADO19690;
XX

DT   12-AUG-2004 (first entry)
XX
DE   Human PRO polypeptide #308.
XX
KW   Human; PRO; immune related disorder; systemic lupus erythematosus;
KW   rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW   systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW   autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW   diabetes mellitus; renal disease; demyelinating disease;
KW   central nervous system; peripheral nervous system;
KW   demyelinating polyneuropathy; Guillain-Barre syndrome;
KW   chronic inflammatory demyelinating polyneuropathy.
XX
OS   Homo sapiens.
XX
XX
PN   WO200404336l-A2.
XX
PD   27-MAY-2004.
XX
PF   06-NOV-2003; 2003WO-US035268.
XX
PR   08-NOV-2002; 2002US-0425235P.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI   Wood WI, Wu TD;
XX
PS   Claim 7; SEQ ID NO 616; 1731pp; English.
XX
CC   The invention relates to human PRO polypeptides and the polynucleotides
CC   encoding them. The polypeptides and polynucleotides are useful for
CC   treating and diagnosing immune related disorders in mammals. The immune
CC   related disorders include systemic lupus erythematosus, rheumatoid
CC   arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC   sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC   haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC   mellitus, immune-mediated renal disease, demyelinating diseases of the
CC   central or peripheral nervous system, demyelinating polyneuropathy,
CC   Guillain-Barre syndrome and chronic inflammatory demyelinating
CC   polyneuropathy. This sequence represents a human PRO polypeptide of the
CC   invention.
XX
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 8; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
              ||||||||:||||||:|||||||||||||||||||||:||||:|||||||||||||| ||
Db   241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPSPSK 313
              |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 13
ADR88370
ID   ADR88370 standard; protein; 313 AA.
XX
AC   ADR88370;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Human PIM 1 protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase; PIM; human.
XX
OS   Homo sapiens.
XX
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
XX
PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-04113998P.
PR   20-SEP-2002; 2002US-04123441P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K, Milburn MV;
XX
PS   Disclosure; SEQ ID NO 9; 186pp; English.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the human PIM 1
CC   protein. This sequence is used to illustrate the method of invention.
XX
SQ   Sequence 313 AA;

Query Match   98.1%; Score 1636; DB 8; Length 313;
Best Local Similarity   97.1%; Pred. No. 1.6e-155;
Matches 304; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

```
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIVKGQVYFRQVRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        |||::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 PFEHDEEIIRGQVYFRQVRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313

RESULT 14
ID   ADP24227 standard; protein; 313 AA.
XX
AC   ADP24227;
XX
DT   18-NOV-2004  (first entry)
XX
DE   PRO polypeptide SEQ ID NO:1405.
XX
KW   PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW   osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW   antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS   Unidentified.
XX
PN   WO200404170-A2.
XX
PD   21-MAY-2004.
XX
PF   30-OCT-2003; 2003WO-US034312.
XX
PR   01-NOV-2002; 2002US-0423394P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI   Wu TD;
XX
DR   WPI; 2004-419628/39.
DR   N-PSDB; ADP24226.
XX
PT   New PRO polypeptides and polynucleotides, useful for treating e.g.
PT   erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT   renal disease, or demyelinating diseases of the central or peripheral
PT   nervous system.
XX
PS   Claim 7; SEQ ID NO 1405; 2940pp; English.

CC   The invention relates to a novel isolated nucleic acid and the PRO
CC   polypeptide encoded by it. A protein of the invention has
CC   antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC   osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC   antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC   of the invention may have a use in gene therapy. The PRO polypeptide, its
CC   agonist, antagonist, or antibody that specifically binds to the
CC   polypeptide is useful for treating an immune related disorder such as
CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, a
CC   juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC   idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, a demyelinating disease of the central or peripheral nervous
CC   system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC   a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC   disease, infectious or autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
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CC   inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC   disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC   disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC   disease, asthma, allergic rhinitis, atopic dermatitis, food
CC   hypersensitivity, urticaria, an immunologic disease of the lung,
CC   eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC   pneumonitis, a transplantation associated disease, graft rejection or
CC   graft-versus-host disease. The present sequence represents a PRO protein
CC   of the invention.
XX
SQ   Sequence 313 AA;

Query Match             98.1%;  Score 1636;  DB 8;  Length 313;
Best Local Similarity   97.1%;  Pred. No. 1.6e-155;
Matches  304;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYGVGPLLGGSGGFGSVVYSGIRVAD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYGVGPLLGGSGGFGSVVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLIKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQVRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        ||||||:::||||||||||||||||||||||||:||||||:|||||||||||||||||:||
Db  241 PFEHDEEIIRGQVYFRQVRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGPSK 313
        |||||||||||||
Db  301 EIHLHSLSPGPSK 313

RESULT 15
ID   ADT07365 standard; protein; 313 AA.
XX
AC   ADT07365;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human protein #1 associated to anticancer compound screening method.
XX
KW   human.
KW   Prophylactic-therapeutic agent; apoptosis inducing agent;
KW   anticancer agent; serine/threonine kinase Pim-1; cancer; solid tumour;
XX
OS   Homo sapiens.
XX
PN   WO200409058-A1.
XX
PD   21-OCT-2004.
XX
PF   05-APR-2004; 2004WO-JP004917.
XX
PR   03-APR-2003; 2003US-0459644P.
XX
PA   (ONCO-) ONCOREX INC.
XX
PI   Kobayashi M, Jian C;
XX
DR   WPI; 2004-748778/73.
DR   N-PSDB; ADT07366.
XX
PT   Screening for a prophylactic-therapeutic apoptosis inducing agent or
```

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PT    enhancer of anticancer agent, comprises use of serine/threonine kinase
PT    Pim-1, its partial peptide or its salt.
XX
PS
PS    Disclosure; SEQ ID NO 1; 93pp; Japanese.
XX
CC
CC    The invention relates to a method of screening a prophylactic-therapeutic
CC    agent for an apoptosis inducing agent or an enhancer of an anticancer
CC    agent. The method involves the use of a serine/threonine kinase Pim-1,
CC    its partial peptide or its salt. Also disclosed is a kit for carrying out
CC    the method of the invention. The method is useful for screening a
CC    prophylactic-therapeutic agent for cancer. The method is also useful for
CC    prophylaxis and/or treatment of cancer, inducing apoptosis, treating a
CC    patient having a solid tumour that is resistant to an anticancer agent
CC    (induced by hypoxia), and for screening a substance that promotes or
CC    inhibits the activity of serine/threonine kinase Pim-1. The present
CC    sequence represents a human polypeptide relating to the present
CC    invention.
XX
SQ    Sequence 313 AA;

Query Match             98.1%;      Score 1636;  DB 8;   Length 313;
Best Local Similarity   97.1%;      Pred. No. 1.6e-155;
Matches 304;  Conservative 6;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1 MLLSKINSLAHLRRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60
          ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||:|
Db      1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVSD 60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIVKGQYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300
          ||||||||||:::||||||||||||||||||:||||||||||||||||||||||||||
Db    241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy    301 EIHLHSLSPSPSK 313
          |||||||||:|||
Db    301 EIHLHSLSPGPSK 313
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Search completed: May 4, 2006, 05:24:47
Job time : 114.667 secs

us-10-705-757-4.rpr

OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:19:22 ; Search time 20.3333 Seconds
 (without alignments)
 1481.107 Million cell updates/sec

Title: US-10-705-757-4
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRRAAPCNDL...........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	1	S26298	protein kinase (EC
2	1636	98.1	313	1	TVHUP1	protein kinase (EC
3	1584	95.0	313	1	TVMSP1	protein kinase (EC
4	876.5	52.5	370	1	S55333	protein kinase pim
5	622	37.3	363	2	T22255	hypothetical prote
6	495	29.7	409	2	T14435	hypothetical prote
7	378	22.7	481	2	I49072	protein kinase - m
8	374	22.4	1101	2	S66730	hypothetical prote
9	374	22.4	1398	2	T13741	hypothetical prote
10	367	22.0	504	2	T10449	probable serine/th
11	366	21.9	1358	1	S33653	probable serine/th
12	361	21.6	512	1	JC1446	serine/threonine-s
13	357.5	21.4	798	2	JC7500	qik protein - chic
14	357	21.4	512	2	S52633	serine/threonine-s
15	357	21.4	651	2	S52244	p69Eg3 protein - A
16	356	21.3	511	1	A56009	serine/threonine-s
17	355	21.3	726	2	T13998	hypothetical prote
18	354.5	21.3	887	2	T20941	hypothetical prote
19	353.5	21.2	469	2	B84644	probable protein k
20	350.5	21.0	504	2	T07415	probable serine/th
21	350	21.0	512	2	T07788	probable serine/th
22	348.5	20.9	472	2	JN023	probable serine/th
23	348	20.9	414	2	B90100	SNF-related kinase
24	344	20.6	513	1	S6004	serine/threonine-s
25	336.5	20.2	445	2	T50802	serine/threonine p
26	336.5	20.2	489	2	T04862	probable serine/th
27	336	20.1	713	2	S27966	probable serine/th
28	336	20.1	1558	2	T29953	hypothetical prote
29	334.5	20.1	1518	2	S37928	probable purine nu
30	333.5	20.0	339	2	S56719	serine/threonine-s
31	333.5	20.0	746	2	S62365	SNF1-related prote
32	333	20.0	435	2	B84707	probable protein k
33	333	20.0	502	2	T02306	probable protein k
34	331.5	19.9	502	2	G86414	probable protein k
35	330	19.8	461	2	T14822	probable serine/th
36	328	19.7	442	2	T48203	hypothetical prote
37	328	19.7	591	2	G01025	serine/threonine p
38	326	19.5	591	2	S54788	serine/threonine p
39	325.5	19.5	774	2	I48609	calcium-stimulated
40	325	19.5	513	1	S60303	serine/threonine-s
41	325	19.5	1246	2	G89287	protein H39E23.1 [
42	324.5	19.5	423	2	T40224	protein kinase - f
43	323.5	19.4	713	2	T37886	probable serine/th
44	322.5	19.3	473	1	S59941	serine/threonine-s
45	321.5	19.3	480	2	A86427	probable serine/th

ALIGNMENTS

RESULT 1
S26298
protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S26298
R;Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
A;Title: Characterization of the testis-specific pim-1 transcript in rat.
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI0000131AD6; EMBL:X63675; NID:g56902; PIL
A;Note: in testis may be involved in signal transduction events of normal germ cell mat
A;Experimental source: testis
A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Accession: S26298
A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; UNIPARC:UPI0000131AD6;
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncoge
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

Query Match 100.0%; Score 1668; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 2.6e-74;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSKINSLAHLRRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLLSKINSLAHLRRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRG 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVVTDFDGTRVSYPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVVTDFDGTRVSYPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy 301 EIHLHSLSPSPSK 313

RESULT 2

Db   301 EIHLHSLSPSPSK 313

```
TVHUP1
protein kinase (EC 2.7.1.37) pim-1 - human
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPARC:UPI00000001060; GB:M27903; NID:g189958; PIDN:
R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene relat
A;Reference number: A46554; MUID:88115604; PMID:3429489
A;Accession: A46554
A;Molecule type: mRNA
A;Residues: 1-313 <MEE>
A;Cross-references: UNIPARC:UPI00000001060; GB:M24779; NID:g1066790; PIDN:AAA81553.1; PID
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
Gene 54, 105-121, 1987
A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
A;Reference number: A27476; MUID:87277423; PMID:3475233
A;Accession: A27476
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI000000149B7C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID
R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
Oncogene Res. 1, 103-112, 1987
A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolo
A;Reference number: I58412; MUID:88217305; PMID:3329709
A;Accession: I58412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-14, 'RA', 17-313 <ZAK>
A;Cross-references: UNIPARC:UPI00000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase homology <KIN>
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

Query Match         98.1%;  Score 1636;  DB 1;  Length 313;
Best Local Similarity   97.1%;
Matches    304;  Conservative    6;  Pred. No. 9.2e-73;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVVYSPPEWIRYHYRGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVVYSPPEWIRYHYRGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        |||||||::|||:||||||||||||||||||||:|||||:||||||||||||||||||:|
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPSPSK 313
        ||||||||||:||
Db  301 EIHLHSLSPGPSK 313
```

RESULT 3

```
TVMSP1
protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.; v
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology w
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g20
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: pim-1
C;Function:
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted

Query Match         95.0%;  Score 1584;  DB 1;  Length 313;
Best Local Similarity   94.2%;
Matches    295;  Conservative    8;  Pred. No. 3e-70;  Mismatches    10;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
        |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEBDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 ELKLIDFGSGALLKDTVYTDFDGTRVVYSPPEWIRYHYRGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVVYSPPEWIRYHYRGHSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
        |||||||::|||:||||||||||||:||||||||||||::|||||:|||||||||||||:
Db  241 PFEHDEEIIKGQVFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPSPSK 313
        ||||||||||:||
Db  301 EIHLHSLSPGSSK 313
```

RESULT 4

```
S55333
protein kinase pim-2 (EC 2.7.1.-) - mouse
```

```
C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1
A;Reference number:
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPROT:Q62070; UNIPARC:UPI0000028629; GB:L41495; NID:g765065; PIDN:
A;Accession: A43093
A;Note: 40K form
A;Molecule type: mRNA
A;Residues: 'M,27-370 <VA2>
A;Cross-references: UNIPARC:UPI000020278BE; GB:L41495; NID:g765065; PIDN:AAA98923.1; PID:
A;Accession: B43093
A;Note: 37K form
A;Molecule type: mRNA
A;Residues: 'M,61-370 <VA3>
A;Cross-references: UNIPARC:UPI000002782BF; GB:L41495; NID:g765065; PIDN:AAA98924.1; PID:
A;Note: 34K form
C;Comment: Pim-2 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
A;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

Query Match      52.5%;   Score 876.5;   DB 1;   Length 370;
Best Local Similarity  58.4%;   Pred. No. 5.4e-36;
Matches 167;   Conservative  40;   Mismatches  74;   Indels   5;   Gaps   2;

Qy     28  GKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVVP  87
               ::: ||||||||||||||||||||||||||||||||| ||| :|| || || ||| ||
Db     81  GKDRAAFEAEYRLGPLLGKGGFGTVFAGHRVTDRRQVAIKVISRNVLGWSTVSDSVTCP  140

Qy     88  MEVVLLKKV--SSGFSGVIRLLDWFERPDSFVLILERREPEVQDLFDFITERGALQEELAR  145
               || ||||| : ||| |||||||||||| :| :|||||||||: ||||||||||||| |
Db    141  LEVALIMKVGEGNGHPGVIRLLDWFETPEGFMLVLERMPAQDLFDYITEKGPLGESCSR  200

Qy    146  SFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTFDGTR  205
               :|| :|| ||||||||||||||||||||| :|| |||| |||||||||||||||||
Db    201  SFFTQVVAAVQHCHARGVVHRDIKDENLLIDLCRGSIKLIDFGSGALLHDEPYTDFDGTR  260

Qy    206  VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIVKGQVYFRQRVSSECQH  265
               ||||||| | |||||||||||||||||||||||||||||| :|| |||||||||||
Db    261  VYSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA  320

Qy    266  LIRWCLSLRPSDRPSFEEIQNHPWMQS---PAEEKPINSSKGSPTP  363
               |||| :|| :||||||||||||||||      || ||||||||
Db    321  LIRRCLAPKPCSRPSLEEILLDPWMQS---PAEEKPINSSKGSPTP  363
```

```
RESULT 5
T22255
hypothetical protein F45H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T22255
R;Percy, C.
submitted to the EMBL Data Library, June 1994
R;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
```

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A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI00001755A4; EMBL:Z34800; PIDN:CAA84323.1
A;Experimental source: UNIPROT:Q62070; UNIPARC:UPI00001755A4; EMBL:Z34800; PIDN:CAA84323.1
A;Gene: CESP:F45H7.4
A;Map position: 3
A;Genetics:
A;Introns: 72/3; 160/3; 310/1
C;Superfamily: protein kinase homology

Query Match      37.3%;   Score 622;   DB 2;   Length 363;
Best Local Similarity  45.7%;   Pred. No. 1.1e-23;
Matches 121;   Conservative  49;   Mismatches  89;   Indels   6;   Gaps   3;

Qy     35  ESQYQVGPLLGSGGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK  94
               :|| ||||||||||||||||||||||||||||||||| :| :|| || || || :||
Db     28  KKNYKLKAELGRGGFGVVYRAVRTCDNALVAVKFIERSNVKEWARI-NGEQVPMEICMLA  86

Qy     95  KVSSGFSGVIRLLDWFERPDSFVLILERREPEVQDLFDFITERGALQEELAR  154
               | : |||| ||||||: :|: ||:||||| |||||||||||||: :||||:
Db     87  KCSK-VRGVIRLLDWYSIPEGFLIVMERRYPCIDMFDFIKGQGKISEDMARFLFRQIAVT  145

Qy    155  VRICHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTFDGTRVYSPPEWIR  214
               |:|:| |||||||||||:||:|||||||||||||||||||:|| || ||||||||||:
Db    146  VHECVQNRVLHRDIKDENTVIDLVTGSTKLIIDFGAAATVLRRSQYSDFQGTRLYCPEWEL  205

Qy    215  YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI----VKGQVYFRQRVSSECQHLIRWC  270
               ||||||||||||||||||||||||||||||||||     :||||| |||||| || ||
Db    206  HSLYIGREAAVWSLGVLLYNSLNGRLPRNEKDICTAHLLGPLPFFVPVSAEVKDLISKC  265

Qy    271  LSLRPSDRPSFEEIQNHPWMQDVLL  295
               | :|||||||||||||||||:||||
Db    266  LTFDPFORCSLEAILNHPWVKQQTL  290
```

```
RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid C06E8.
A;Reference number: Z18350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI0000017B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN:
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C06E8.3
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

Query Match      29.7%;   Score 495;   DB 2;   Length 409;
Best Local Similarity  35.3%;   Pred. No. 1.6e-17;
Matches 110;   Conservative  57;   Mismatches 129;   Indels  16;   Gaps   6;

Qy      1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGGFGSVYSGIRVAD  60
               |: || |: |:: | |||  :|:|||  |::|||||||||||||||||||||||||||
Db      1  MIRKLQDLIAVCCSYQVDFLHEKK------HSVKEFKRKYEVLDEIGRGGFGVIVEATRQD  56

Qy     61  -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLI  119
                ||||||||| || || |||||||| |||: ||: || :| || |||||||||| |||
Db     57  GQQPVAVKFVQHGHVRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFIV  114

Qy    120  LERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLN  178
               ||:||||||||||||||||||:|  :||| || || || || |||||||||||| :
Db    115  MERPANCMDLFDMVSVHGPLNEDMGKFIFKQVTTVFRNMYSKHGLLHRDIKDENLIVAMN  174

Qy    179  RGELKLIDFGSGALLKDTVYTFDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG  238
               ||||||||||| ||||:|||| |:|:||||||||||||||| ||||||||||||||||
Db    175  TGEVKLVDFGGATAYAEKATKEFQGTRSYCPPEWFRDQLYPLEATSNWSLGVLFILTG  234
```

```
Qy   239 DIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQ------ 291
             ||::|| ::::||||||||||||||||||||||||||||||||||||||
Db   235 KLPFRNEIQICLGNVKPPDLSKEVCQLVKSCLTTSTSARASLAQIAAHPWMETDKPFFG 294

Qy   292 -DVLLPQATAEI 302
             |||| ||
Db   295 GDLTFEEALMEI 306
```

RESULT 7
I49072
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
A;Reference number: I49072
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
Mech. Dev. 48, 153-164, 1994
A;Reference number: I49071; MUID:95200798; PMID:7893599
A;Accession: I49072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
C;Keywords: ATP
F;71-324/Region: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

Query Match   22.7%; Score 378; DB 2; Length 481;
Best Local Similarity 33.2%; Pred. No. 8.4e-12;
Matches 97; Conservative 53; Mismatches 116; Indels 26; Gaps 10;

```
Qy     9 LAHLRAAPCNDLHANKLAPGKEKEPLE-SQYQVGPLLGSSGGFGSSV-YSGIRVADNLPVAI 66
             |:|| :||| ||
Db    51 MSFRAVPS---------GTGRSQKPLRVGFYDVERTLGKGNFAVVKLRGHRVI-KTQVAI 101

Qy    67 KHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLILERPPV 126
             :|:||||||||||||||||||||||||||||||||||||||||||||||
Db   102 KIIDKTRL----DSSNLEKIYREVQLMKLLN--HPNIIKLYQVWETKDMLIYVTEFAKN- 154

Qy   127 QDLFDFITERGALQEELARSFFWQVLEAVRHCHNCNCGVLHRDIKDENILIDLNRGELKLID 186
             | ::| :||||||||||||||||||||||||||||||||||||||||||||||
Db   155 GEMFDYLTSNGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLDSNM-DIKLAD 213

Qy   187 FGSGALLK-DTVYTDFDGTRVSYPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHD 245
             ||||||| :|| ||||||||||||||||||||||||||||||||||||||||||
Db   214 FGFGNFYKPGEPLSTCVSGSPPYAAPEVFEGKEYEGPQLDVWSLGVVLYLVCCGSLPFDGP 273

Qy   246 ----EEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
             :::|||||||||||||||||||||||||||||||||||||||||
Db   274 NLPTLRQRVLEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRWMQ 325
```

RESULT 8
S66730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI00012DF35; EMBL:Z74788; NID:g1419846; PI
A;Experimental source: strain S288C
C;Genetics:
A;Cross-references: SGD:S0005405
A;Map position: 15L
C;Keywords: ATP

F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

Query Match   22.4%; Score 374; DB 2; Length 1101;
Best Local Similarity 32.2%; Pred. No. 2.6e-11;
Matches 86; Conservative 62; Mismatches 103; Indels 16; Gaps 6;

```
Qy    36 SQYQVGPLLGSSGGFGSSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVLL 93
             ...
Db   839 SDFTILQVWGEGAYGKVNLCIHNREHIVVIKMFKERILVDDTWVRDRKLGTIPSEIQIM 898

Qy    94 KKVS-SGFSGVIRLLDWFERPDSFVLILERPPVQ------DLFDFITERGALQEELARS 146
Db   899 ATLNKNSQENILKLLDFEDDDYYI---ETPVHGETGSIDLFDVIEFKKDMVEHEARKL 954

Qy   147 FFWQVLEAVRHCHNCNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRV 206
Db   955 VFKQVVASIKHLHDQGIVHRDIKDENVIVD-SHGFVKLIDFGSAAYIKSGPFDVFVGTMD 1013

Qy   207 YSPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHDEEIVKGQVYF--RQRVSSECQ 264
Db  1014 YAAPEVLGSSYGKPQDIWALGVLLYTIIYKENPYYNIDEILEGELRFDKSEHVSECI 1073

Qy   265 HLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
Db  1074 SLIKRILTREVDKRPTIDEIYEDKWLK 1100
```

RESULT 9
T13741
hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217668
A;Accession: T13741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPARC:UPI00000820A3; EMBL:AL031765; NID:e1371523;
C;Genetics:
A;Cross-references: FlyBase:FBgn0000667
A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
A;Note: EG:22E5.8

Query Match   22.4%; Score 374; DB 2; Length 1398;
Best Local Similarity 33.0%; Pred. No. 3.2e-11;
Matches 91; Conservative 57; Mismatches 110; Indels 18; Gaps 9;

```
Qy    29 KEKEPLE-SQYQVGPLLGSSGGFGSSV-YSGIRVADNLPVAIKHVEKDRISDWGELPNGTRV 86
             ...
Db   131 KLKEPMRVGFYDIERTIGKGNFAVVKLARHRITKN-EVAIKIIDKSQL---DQTNLQKV 185

Qy    87 PMEVVLLKKVSSGGFSGVIRLLDWFERPDSFVLILERPPVQDLFDFITERGALQEELARS 146
Db   186 YREVEIMKRLK--HPHIIKLYQVWETKNMIYIVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy   147 FFWQVLEAVRHCHNCNCGVLHRDIKDENILIDLNRGELKLIDFG-SGALLKDTVYTDFDGTR 205
Db   243 KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP 301

Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILILYDMVCGDIPFEHD-----EEIVKGQVYFRQRV 259
Db   302 PYAAPEVFEGKQYTGPEIDIWSLGVVLYLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM 361

Qy   260 SSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLL 295
Db   362 SSECEHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397
```

RESULT 10
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
A;Accession: T10449
A;Reference number: Z17020
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
C;Accession: T10449
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI000000A4B92; EMBL:Y10036
A;Residues: 1-504 <GUM>
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T10449
A;Reference number: Z17020
A;Experimental source: cv. Masterpiece; cotyledon
C;Genetics:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein homology; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match 22.0%; Score 367; DB 2; Length 504;
Best Local Similarity 34.4%; Pred. No. 3e-11;
Matches 90; Conservative 51; Mismatches 105; Indels 16; Gaps 8;

```
Qy    38 YQVGPLLGSSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
          | ::|:| |    ||:||  :||:||||:|:|||| :|  | :::| |||||||||||||||||
Db     8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKV---LDMEEKVRREIKILRLFM 64

Qy    98 SGFGSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
          ||    :|:|:|:|:|:|:   ||:| |:|:  |:|: |:| | ||:| |   |:|| |
Db    65 --HPHIIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEAARNFFQQIISGVEY 121

Qy   158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH 216
          ||:||:||||||||||||||| ||||||||||| ||||||:|:|  |||||||||||| |
Db   122 CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK 180

Qy   217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSECQHLIRW 269
          | ||| ||| |:| :|  |:  |::|||||   ||| ||  | || | :::|:   ::
Db   181 LYAGPEVDVWSCCVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy   270 CLSLRPSDRPSFEEIQNHPWMQ 291
          |:|:|||||||||||||||
Db   240 MLVVDPMKRITPEIRQHPWFQ 261
```

RESULT 11
S33653
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
A;Accession: S33653
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc
A;Reference number: S33653; MUID:93111122; PMID:8322517
A;Accession: S33653
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a 3
A;Reference number: S36711
A;Accession: S36717
A;Molecule type: DNA
A;Residues: 1-864, 867-1358 <QUE>
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
Yeast 8, 133-145, 1992

RESULT 12
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
A;Accession: JC1446
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protei
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI00012DE43; GB:M93023; NID:g165599; PIDN
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase
A;Reference number: S58266
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>

Query Match 21.9%; Score 366; DB 2; Length 1358;
Best Local Similarity 33.3%; Pred. No. 7.7e-11;
Matches 86; Conservative 56; Mismatches 100; Indels 16; Gaps 6;

```
Qy    44 LGSGGFGSSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SGF 100
          |||| |||| :|||||||| ||||||:||:|   ||||||||||||||| || || |  ||
Db  1104 MGEGAYGKVNLCIHKKNRVIVIRKERILVDTWVRDRKLGTIPSEIQIMATLNKKPH 1163

Qy   101 SGVIRLLDWFERPDSFVLILERPEPVQ------DLFDFITERGALQEELARSFFWQVLEA 154
          ||::||:|:|:|:||||::|::|       |:||||| ||| |||::| |   |:||
Db  1164 ENIRLLDFFEDDDYYI----ETPVHGETGCILFDLLEFKTNMTEFEAKLIFKQVVAG 1219

Qy   155 VRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIR 214
          || |:||:|||||||||| |:|| |:|||||||:| |||||:|:|  || || |||||
Db  1220 IKIHLHDQGIVHRDIKDENVIVD-SKGFVKIIDFGSSAAYVKSGPEDVFVGTIDYAAPEVLG 1278

Qy   215 YHYRHGRSAAVWSLGILLYDMVCGDIPFEHDEEIVKGQVYFR--QRVSSECQHLIRWCLS 272
          |||:|| ||| |:| :|  | | ||||||||  ||:|  | |  |: |:||:   |:  |
Db  1279 GNPYEGGQPQDIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN 1338

Qy   273 LRPSDRPSFEEIQNHPWM 290
          ||| ||||||||||||
Db  1339 RCVPKRPTIDDINNDKWL 1356
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A;Cross-references: UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g9288909; PIDN:CAA60529.1; PI
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
Plant. Mol. Biol. 29, 551-565, 1995
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI000009DEE0; EMBL:X86966; NID:g9288909; PIDN:CAA60529.1; PI
A;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Genetics:
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; protein kinase; serine/threonine-specific protein kinase
F;25-33/Region: protein kinase ATP-binding motif <KIN>
F;48,67,142,144/Active site: Lys, Glu, Lys, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

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Db  26 YDIERTLGKGNFAVVKLARHRVTKTQVAIKIIDKTRL----DPSNLEKIIYREVOIMKLN 81
Db  98 SGFESGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARSFFWQVLEAVRH 157
Db  82 --HPHIIKLYQVMETKDMLIYIVTEFAKN-GEMFDHLISNGHLSESEARKKFWQILSAVEY 138
Db 158 CHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
Db 139 CHSHHIVHRDLKTENLLLDANM-NIKLADFGFGNFYKSGGEPLSTWCGSPPYAAPEVFGCK 197
Qy 217 RYHGRSAAVWSLGILLLYDMVCGDIPFEHD------EEIVKGQVYFRQRVSSECQHLIRWC 270
Db 198 EYEGHPLDIWSLGVVLYVLVCGSLPFDGDNLPLRQRVLEGRFRIPYEMSEDCETLIRM 257
Qy 271 LSLRPSDRPSFEEIQNHPWMQ 291
Db 258 LVVDETKRITISQIKQHKMQ 278
```

RESULT 14
T52633
serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis t
N;Alternate names: SNF1 protein kinase omolog AKIN11
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004
C;Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein ki
A;Reference number: Z25116; MUID:99238528; PMID:10220464
A;Accession: T52633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D; EMBL:X99279; PIDN:CAA67671.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: AKIN11
A;Function: EC 2.7.1.-; serine/threonine-specific protein kinase
A;Description: SNF1 mutations in yeast
complements SNF1-related protein kinase; protein kinase homology
C;Superfamily: SNF1-related protein kinase; serine/threonine-specific protein kinase
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match   21.6%; Score 361; DB 1; Length 512;
Best Local Similarity   33.6%; Pred. No. 5.9e-11;
Matches 90; Conservative 51; Mismatches 111; Indels 16; Gaps 8;

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Qy  32 EPLESQYQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db  13 ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAVAIKILNRRKIKN--MEMEKVRREIK 69
Qy  92 LLKKVSSGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARSFFWQV 151
Db  70 ILRLFM--HPHIIRLYEVIETPDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126
Qy 152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db 127 ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185
Qy 211 EWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSEC 263
Db 186 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPCA 244
Qy 264 QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
Db 245 RDLIPRMLVVDPMKRVTIPEIRQHPWFQ 272
```

RESULT 13
JC7500
qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Reference number: JC7500
A;Contents: Embryo fibroblasts
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: UNIPROT:Q9IAB8; UNIPARC:UPI000004792; GB:AF219232
A;Title: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases, h
C;Genetics:
A;Gene: qik
C;Keywords: protein kinase

Query Match   21.4%; Score 357; DB 2; Length 512;
Best Local Similarity   33.6%; Pred. No. 9.2e-11;
Matches 90; Conservative 52; Mismatches 110; Indels 16; Gaps 8;

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Qy  32 EPLESQYQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db  14 ESILPNYKLGKTLGIGSFGKVKIAEHVVTGHKVAVAIKILNRRKIKN--MEMEKVRREIK 70
Qy  92 LLKVSSGFSGVIRLLDWFERPDSFVLILERPEVQDLFDFITERGALQEELARSFFWQV 151
Db  71 ILRLFM--HPHIIRQYEVETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI 127
Qy 152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db 128 ISGVEYCHRNMVVHRDLKPENLLLD-SRCNIKIADFGLSNIMRDGHFLKTSCGSPNYAAP 186
Qy 211 EWIRYHRYHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------VKGQVY-FRQRVSSEC 263
Db 187 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA 245
Qy 264 QHLIRWCLSLRPSDRPSFEEIQNHPWMQ 291
Db 246 RDLIPRMLIVDPVKRITIPEIRQHRWFQ 273
```

RESULT 15
S52244
p69Bg3 protein - African clawed frog

Query Match   21.4%; Score 357.5; DB 2; Length 798;
Best Local Similarity   32.2%; Pred. No. 1.3e-10;
Matches 84; Conservative 51; Mismatches 111; Indels 15; Gaps 6;

```
Qy  38 YQVGPLLGSGGFGSSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
```

C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 05-Oct-2004
C;Accession: S52244
R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A;Description: Eg3, selected by differential screening encodes a new Xenopus protein kin
A;Reference number: S52243
A;Accession: S52244
A;Accession: S52243
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-651 <ROG>
A;Cross-references: UNIPROT:Q91821; UNIPARC:UPI000017A463; EMBL:Z17205; NID:g609283; PID
C;Keywords: ATP
F;11-265/Domain: protein kinase homology <KIN>
F;19-27/Region: protein kinase ATP-binding motif

Query Match   21.4%;   Score 357;   DB 2;   Length 651;
Best Local Similarity   34.1%;   Pred. No. 1.1e-10;
Matches   92;   Conservative   53;   Mismatches   103;   Indels   22;   Gaps   8;

```
Qy     32 EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV  91
             | |: | :|:||||   :  : || || |:  |||  :||::  ||:  | | |:
Db      7 EELLKYYELHETVGTGGFAKVKLASHLITGEKVAIKIMDKESLGD--DLP---RVKTEID  61

Qy     92 LLKKVSSGFSGVIRLLDWFERPDSFVLLLERPEPVQDLLFDFITERGALQEELARSFFWQV 151
             |||:| :  |:|: |: | :|:  ::|: |  || :||  | || |: ||:
Db     62 AMKNLS--HQHVCRLYHVIETPKKIFMVLEYC--PGGELFDYIIAKDRLTEEEARVFFRQI 118

Qy    152 LEAVRHCHNCGVLHRDIKDENILIDLNRGELKLIDFGSSGALLKDTVYTDFD----GTRV 206
          : ||: | | : :| |||  ||| :||: ||||||: | ||:  ||:||       |:
Db    119 VSAVAYIHSQGYAHRDLKPENLLIDEDQ-NLKLIDFGLCAKPKGGL--DYHLMTCCGSPA 175

Qy    207 YSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIVKGQVYFRQRVS 260
           |||:|| | |::| : :|:| |:|:|:|:||: ||:     :: |:|:
Db    176 YAAPELIQGKAYIGSEADIWSMGVLMYALMCGYLPFDDDNVMVLYKKIMRGKYEIPKWLS 235

Qy    261 SECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
          :  | | : || : ||| :  | |||||
Db    236 PGSVLLSQMMQVDPKKRITVKHLLNHPWL 265
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Search completed: May 4, 2006, 05:25:52
Job time : 21.3333 secs

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OM protein - protein search, using sw model
                    GenCore version 5.1.7
            Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:       May 4, 2006, 05:12:40 ; Search time 122 Seconds
                            (without alignments)
                            1810.085 Million cell updates/sec

Title:        US-10-705-757-4
Perfect score: 1668
Sequence:     1 MLLSKINSLAHLRAAPCNDL..........LLPQATAEIHLHSLSPSPSK 313

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:    2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     UniProt_05.80:*
               1: uniprot_sprot:*
               2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Name	Description
1	1668	100.0	313	1	P26794	PIM1_RAT	rattus norv
2	1638	98.2	313	1	Q95J0	PIM1_FELCA	felis silve
3	1636	98.1	313	1	P11309	PIM1_HUMAN	homo sapien
4	1630	97.7	313	1	Q57H7	Q57H7_HUMAN	homo sapien
5	1589	95.3	313	2	Q8NP9	Q8NP9_BOVIN	bos taurus
6	1589	95.3	313	2	Q8CFN8	Q8CFN8_MOUSE	mus musculu
7	1584	95.0	313	2	P06803	PIM1_MOUSE	mus musculu
8	1137	68.2	323	1	Q9PU85	PIM1_COTJA	coturnix co
9	1135	68.0	326	2	Q86V86	PIM3_HUMAN	homo sapien
10	1132.5	67.9	326	1	P58750	PIM3_MOUSE	mus musculu
11	1131.5	67.8	326	1	Q4VBM2	PIM3_RAT	rattus norv
12	1131.5	67.8	380	2	O70444	O70444_RAT	rattus norv
13	1119	67.1	325	2	Q8111X8	Q8111X8_MOUSE	mus musculu
14	1102.5	66.6	318	2	Q66III	Q66III_XENTR	xenopus tro
15	1102.5	66.6	323	1	Q91822	PIM3_XENLA	xenopus lae
16	1098	65.8	337	2	Q5U489	Q5U489_XENLA	xenopus lae
17	1053	63.1	316	2	Q4STF0	Q4STF0_TETNG	tetraodon n
18	876.5	52.5	311	2	Q8R2P0	Q8R2P0_MOUSE	mus musculu
19	876.5	52.5	370	1	Q62070	PIM2_MOUSE	mus musculu
20	866.5	51.9	311	2	Q9P1W9	PIM2_HUMAN	homo sapien
21	861	51.6	310	2	Q7ZVJ5	Q7ZVJ5_BRARE	brachydanio
22	858	51.4	310	2	Q7ZVU5	Q7ZVU5_BRARE	brachydanio
23	853	51.1	310	1	Q8JFW9	Q8JFW9_BRARE	brachydanio
24	851	51.0	310	1	Q6D152	PIM1_BRARE	brachydanio
25	796.5	47.8	288	2	Q4TDC2	Q4TDC2_TETNG	tetraodon n
26	716.5	43.0	221	2	Q8R1Z0	Q8R1Z0_MOUSE	mus musculu
27	628	37.6	500	2	Q61JB7	Q61JB7_CAEBR	caenorhabdi
28	622	37.3	441	2	Q20443	Q20443_CAEEL	caenorhabdi
29	506	30.3	566	2	Q61228	Q61228_CAEBR	caenorhabdi
30	495	29.7	378	2	Q8T3F1	Q8T3F1_CAEEL	caenorhabdi
31	495	29.7	566	2	Q17737	Q17737_CAEEL	caenorhabdi
32	440	26.4	270	2	Q5SPE4	Q5SPE4_BRARE	brachydanio
33	421	25.2	416	2	Q4RFY6	Q4RFY6_TETNG	tetraodon n
34	421	25.2	465	2	Q5SPF6	Q5SPF6_BRARE	brachydanio
35	419.5	25.1	134	2	Q6P2J9	Q6P2J9_HUMAN	homo sapien
36	409	24.5	281	2	Q5SV44	Q5SV44_BRARE	brachydanio
37	403	24.2	125	2	Q6Q2K5	Q6Q2K5_CANFA	canis famil
38	393.5	23.6	268	2	Q5SPP9	Q5SPP9_BRARE	brachydanio
39	391	23.4	1385	2	Q5RH93	Q5RH93_BRARE	brachydanio
40	390.5	23.4	578	1	Q5PQT0	PASK_MOUSE	rattus norv
41	390	23.4	1383	2	Q641K5	Q641K5_MOUSE	mus musculu
42	388.5	23.3	658	2	Q5SPP7	Q5SPP7_BRARE	brachydanio
43	384.5	23.1	261	2	Q8CEE6	Q8CEE6_MOUSE	mus musculu
44	384.5	23.1	261	2	Q5SPQ2	Q5SPQ2_BRARE	brachydanio
45	384	23.0	463	2	Q5RG24	Q5RG24_BRARE	brachydanio

ALIGNMENTS

RESULT 1
PIM1_RAT

```
PIM1_RAT     P26794     STANDARD;      PRT;   313 AA.

ID   PIM1_RAT     STANDARD;      PRT;   313 AA.
AC   P26794;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=92319652; PubMed=1620615;
RA   Wingett D., Reeves R., Magnuson N.S.;
RT   "Characterization of the testes-specific pim-1 transcript in rat.";
RL   Nucleic Acids Res. 20:3183-3189(1992).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to Rp9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; X63675; CAA45214.1; -; mRNA.
DR   PIR; S26298; S26298.
DR   SMR; P26794; 32-308.
DR   Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR   RGD; 3330; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN        38    290       Protein kinase.
FT   NP_BIND       44     52       ATP (By similarity).
FT   ACT_SITE     167    167       Proton acceptor (By similarity).
FT   BINDING       67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35631 MW;  D5757DA9F1821BF9 CRC64;
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Qy   Query Match   100.0%; Score 1668; DB 1; Length 313;
      Best Local Similarity 100.0%; Pred. No. 3.2e-115;
      Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIVKGQVYFRQRVVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300

Qy   301 EIHLHSLSPSPSK 313
          |||||||||||||
Db   301 EIHLHSLSPSPSK 313

RESULT 2

ID   PIM1_FELCA   STANDARD;   PRT;   313 AA.
AC   Q5SLJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
RT   "The cDNA sequence of the feline pim-1 oncogene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; AB073748; BAB71752.1; -; mRNA.
DR   SMR; Q5SLJ0; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   Proton acceptor (By similarity).
FT   BINDING   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35686 MW; C0BE268D63886967 CRC64;

Qy   Query Match   98.2%; Score 1638; DB 1; Length 313;
      Best Local Similarity 97.4%; Pred. No. 5.3e-113;
      Matches 305; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRTAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLIDLNRG 180

Qy   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIRGQVFFRQRVVSSECQHLIRWCLALRPSDRPSFEEIQNHPWMQDVLLPQETA 300
          ||||||| ||| |:|||||||||||||||||||:|||||||||||||| |||||||| ||
Db   241 PFEHDEEIVKGQVYFRQRVVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300

Qy   301 EIHLHSLSPGPSK 313
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Db   301 EIHLHSLSPSPSK 313

RESULT 3

ID   PIM1_HUMAN   STANDARD;   PRT;   313 AA.
AC   P11309; Q96RG3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA   Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT   "Primary structure of the putative human oncogene, pim-1.";
RL   Gene 90:303-307(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA   Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT   "The cDNA sequence and gene analysis of the human pim oncogene.";
RL   Gene 54:105-111(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88212305; PubMed=3329709;
RA   Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA   Berns A.;
RT   "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT   and immunological identification of the in vitro synthesized PIM-1
RT   protein.";
RL   Oncogene Res. 1:103-112(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.

Qy   Query Match   100.0%; Score 1668; DB 1; Length 313;

Qy   301 EIHLHSLSPSPSK 313
          |||||||||||||
Db   301 EIHLHSLSPSPSK 313

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RX   MEDLINE=88115604; PubMed=3429489;
RA   Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT   "Cloning and characterization of the human PIM-1 gene: a putative
RT   oncogene related to the protein kinases.";
RL   J. Cell. Biochem. 35:105-112(1987).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [8]
RP   CHARACTERIZATION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [9]
RP   FUNCTION.
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=22567470; PubMed=12680209;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA   Johnson T., Lilly M.B., Kraft A.S.;
RT   "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RT   localization is necessary for its biologic effects.";
RL   Anticancer Res. 23:167-178(2003).
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC       cells. May affect the structure or silencing of chromatin by
CC       phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC       hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIMID261.html".
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DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; mRNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAA81555.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU00327; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWS; X-ray; A=1-313.
DR   PDB; 1YHS; X-ray; A=33-305.
DR   PDB; 1YI3; X-ray; A=33-305.
DR   PDB; 1YI4; X-ray; A=33-305.
DR   PDB; 1YWV; X-ray; B=1-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   PDB; 2BIK; X-ray; B=1-313.
DR   PDB; 2BZH; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   MIM; 164960; -.
DR   H-InvDB; HIX0005835; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
FT   CONFLICT     15     15       AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA;  35686 MW;  35BA76D3668E69A3 CRC64;

Query Match   98.1%;  Score 1636;  DB 1;  Length 313;
Best Local Similarity   97.1%;
Matches  304;  Conservative   6;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVlIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVIIL  120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||.
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLRG  180

Qy  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSIGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSIGILLYDMVCGDI  240

Qy  241  PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300
         |||||||||.:|||.:||||||||||||||||.||||||||.||||||||||||||||.|
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPSPSK  313
         |||||||||||||
Db  301  EIHLHSLSPSPSK  313
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Db   301 EIHLHSLSPGPSK 313

Left column (RESULT 4)

RESULT 4
Q5T7H7_HUMAN
ID   Q5T7H7_HUMAN PRELIMINARY;   PRT;   313 AA.
AC   Q5T7H7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (Proviral integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL353379; CAI20116.1; -; Genomic_DNA.
DR   SMR; Q5T7H7; 32-308.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004672; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Serine/threonine-protein kinase.
SQ   SEQUENCE   313 AA;   35686 MW;   35BA76D3668D69A3 CRC64;

Query Match   98.1%; Score 1636; DB 2; Length 313;
Best Local Similarity   97.1%;
Matches 304; Conservative   6; Pred. No. 7.4e-113; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||:|:|| ||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIRGQVFFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
          |||||||:|||||||||||||||||||||:||||:||||||||||||||||||||||
Db 241 PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLARPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGPSK 313
          |||||||||||||
Db 301 EIHLHSLSPGPSK 313

Right column (RESULT 5)

RESULT 5
PIM1_BOVIN
ID   PIM1_BOVIN   STANDARD;   PRT;   313 AA.
AC   Q9NP9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   Vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF259078; AAF67200.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMR; Q9NP9; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA;   35630 MW;   9EF40229A847AD47 CRC64;

Query Match   97.7%; Score 1630; DB 1; Length 313;
Best Local Similarity   97.1%;
Matches 304; Conservative   6; Pred. No. 2.1e-112; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||:|:|| ||||||||||||||||||||||||||||||||:|
Db   1 MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG 180

Qy 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

RESULT 6

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Db      301 EIHLHSLSPGPSK 313

Qy      301 EIHLHSLSPSPSK 313

Db      241 PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
            |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||
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ID   Q8CFN8_MOUSE   PRELIMINARY;   PRT;   313 AA.
AC   Q8CFN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Proviral integration site 1.
GN   Name=Pim1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX   MEDLINE=22238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RG   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RG   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Eye;
RG   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
DR   EMBL; BC042885; AAH42885.1; -; mRNA.
DR   EMBL; BC053019; AAH53019.1; -; mRNA.
DR   EMBL; BC055316; AAH55316.1; -; mRNA.
DR   SMR; Q8CFN8; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Transferase;
KW   Serine/threonine-protein kinase.
SQ   SEQUENCE 313 AA; 35451 MW; 1294F16A03B7C7D7 CRC64;

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Query Match             95.3%;
Best Local Similarity   94.6%;
Matches   296;  Conservative   8;  Mismatches   9;  Indels   0;  Gaps   0;

Qy      1   MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYGPLLGSGGFGSVYSGIRVAD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1   MLLSKINSLAHLRAAPCNDLHATKLAAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy      61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy      121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHCNCGVLHRDIKDENLILIDLNRG 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHCNCGVLHRDIKDENLILIDLSRG 180

Qy      181 ELKLIDFGSGGALLKDTVTTPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 EIKLIDFGSGGALLKDTVTTPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy      241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQETA 300
            |||||||||:||||||||||||||||||||||||||||:||||||||||||||| ||||
Db      241 PFEHDEEIIKGQVFFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy      301 EIHLHSLSPSPSK 313
            |||||||| ||||
Db      301 EIHLHSLSPGPSK 313
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RESULT 7

ID   PIM1_MOUSE   STANDARD;   PRT;   313 AA.
AC   P06803;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
RA   Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
RA   Domen J., van Beveren C., Berns A.;
RT   "The primary structure of the putative oncogene pim-1 shows extensive
RT   homology with a protein kinase.";
RL   Cell 46:603-611(1986).
RN   [2]
RP   INTERACTION WITH RP9.
RX   MEDLINE=20389540; PubMed=10931201;
RA   Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA   Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT   "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL   Eur. J. Biochem. 267:5168-5178(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).

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CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC       leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
```

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DR   EMBL; M13945; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1A06.
DR   SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN    38    290   Protein kinase.
FT   NP_BIND   44    52    ATP (By similarity).
FT   ACT_SITE  167         Proton acceptor (By similarity).
FT   BINDING   67          ATP (By similarity).
SQ   SEQUENCE   313 AA;  35537 MW;  79F4779E9DC8DC16 CRC64;

Query Match    95.0%;  Score 1584;  DB 1;  Length 313;
Best Local Similarity   94.2%;
Matches  295;  Conservative  8;  Mismatches  10;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
         ||||||||||||||||||||| ||||||||||||||||:||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAARPCNDLHATKLAPGKEKEPLESQVGPLLGSGGFGSVYSGIRVAD    60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDSFVLIL   120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDPSFVLL   120

Qy  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||:
Db  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180

Qy  181  ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EIKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240

Qy  241  PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA  300
         ||||||||:||||:||:||||||||||:|||||||||||||||||:|||||||:|||:
Db  241  PFEHDEEIIKGQVFFRQVTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS  300

Qy  301  EIHLHSLSPGSSK  313
         |||||||||| ||
Db  301  EIHLHSLSPSPSSK  313
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RESULT 8
PIM3_COTJA
ID   PIM3_COTJA     STANDARD;      PRT;   323 AA.
AC   Q9PUB5;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=PIM3; Synonyms=PIM-3;
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
```

```
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
```

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DR   EMBL; AJ310845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMART; SM00220; S_TKc; 1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN    40    291   Protein kinase.
FT   NP_BIND   46    54    ATP (By similarity).
FT   ACT_SITE  168         Proton acceptor (By similarity).
FT   BINDING   69          ATP (By similarity).
SQ   SEQUENCE   323 AA;  36597 MW;  E2A4FA20B6F63996C CRC64;

Query Match    68.2%;  Score 1137;  DB 1;  Length 323;
Best Local Similarity   67.3%;
Matches  212;  Conservative  43;  Mismatches  56;  Indels  4;  Gaps  4;

Qy    1  MLLSKINSLAHL-RAAPCNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIRV   58
         |||||||||     || ||    |||    | :||||||    |||||:||||||||||||:
Db    1  MLLSKFGSLAHICSPASMDHLPVKILPPVKEKPFDKYYQVGSVLGSGGFGTVYAGSRT    60

Qy   59  ADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVL  118
         ||:|||||||:||:||||  || ||| :||:||:|||    ||||:| |||||: ||||
Db   61  ADGLPVAVKHVVKERVTEWGTI-GGVMVPLEIVLLKKVSGFRGVIKLLDWYERPDGFLI  119

Qy  119  ILERREPVQODLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN  178
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  120  VMERPELVKDLFDFITEKGALDEDTARGFRQVLEAVRHCICGCVVHRDIKDENLLVDLR  179

Qy  179  RGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG   238
         ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db  180  TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDMVCG   239

Qy  239  DIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM-QDVLLPQ  297
         :||||||||||:||||||:||||||||||||||||||||||||||||:|||| ||:||||
Db  240  DIPFEQDEEILKGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS  299

Qy  298  ATAEIHLHSLSPSPS  312
         ||  ||||||||||::
Db  300  EDCDIRLRTLDTDVS  314
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RESULT 9
PIM3_HUMAN
ID   PIM3_HUMAN     STANDARD;      PRT;   326 AA.
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AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15540201; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   IDENTIFICATION FROM ESTS.
RX   MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA   Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
RT   "Consistency checks for characterizing protein forms.";
RL   Comput. Biol. Chem. 27:29-35(2003).
CC   -!- FUNCTION: May be involved in cell cycle progression and anti-
CC       apoptosis process. Implicated in proliferation of human hepatoma
CC       cell lines.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC       thymus, and small intestine. Expressed in human hepatoma cell
CC       lines but not in normal liver tissues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; AB111795; BAD42438.1; -; mRNA.
DR   EMBL; BC052239; -; NOT ANNOTATED CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pKin_AS.
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```
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN        40    293       Protein kinase.
FT   NP_BIND       46     54       ATP (By similarity).
FT   ACT_SITE     170    170       Proton acceptor (By similarity).
FT   BINDING       69     69       ATP (By similarity).
SQ   SEQUENCE    326 AA;  35863 MW;  41FDF9DD2467A162 CRC64;
```

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Query Match             68.0%;  Score 1135;  DB 1;  Length 326;
Best Local Similarity   69.6%;  Pred. No. 8.7e-76;
Matches  220;  Conservative  34;  Mismatches  52;  Indels  10;  Gaps  7;

Qy      1  MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR  57
           |||||||||||||| :: :|: ||:|||||||| :||||:||:||||||||||||||:|||
Db      1  MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYAGSR  59

Qy     58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS  115
           ||||||||||||||||||||||||| :||||| |||||||    :||||||||||||||||
Db     60  IADGLPVAVKHVVKERVTEWGSL-GGATVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG  118

Qy    116  FVILLERPEPVQDLFDFITERGALOEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI  175
           |:||||||||||||||||||||||||||||||:|||:|||||||||||||||||||||||
Db    119  FLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDENLLV  178

Qy    176  DLNRGELKLIDFGSGALLKDTVITDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
           ||||||||||||||||||:|||:|||||||||||||||||||||:|| ||||||||||||
Db    179  DLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM  238

Qy    236  VCGDIPFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWM--QDV  293
           ||||||||||||:|||||||||||| :|||| ||||||||||||||||:|||||||  |||
Db    239  VCGDIPFEQDEEILRGRLLFRRRVSPECCQLIRWCLSLRPSERPSLDQIAAHPWMLGADG  298

Qy    294  LLPQATAEIHLHSLSP  309
           |:: :|: | |: ||
Db    299  GAPE-SCDLRLCTLDP  313
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RESULT 10
PIM3_MOUSE
ID   PIM3_MOUSE              STANDARD;      PRT;    326 AA.
AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.

DR EMBL; BC017621; AAH17621.1; -; mRNA.
DR EMBL; BC026639; AAH26639.1; -; mRNA.
DR HSSP; Q03565; 1HOW.
DR Ensembl; ENSMUSG00000035828; Mus musculus.
DR MGI; MGI:1355297; Pim3.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase_AS.
DR InterPro; IPR002290; Ser/Thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation; Transferase;
KW Serine/threonine-protein kinase.
FT DOMAIN   40   293   Protein kinase.
FT NP_BIND   46   54   ATP (By similarity).
FT ACT_SITE   170   Proton acceptor (By similarity).
FT BINDING   69   ATP (By similarity).
SQ SEQUENCE   326 AA; 35970 MW; DD68CBF46354851E CRC64;

Query Match   67.9%; Score 1132.5; DB 1; Length 326;
Best Local Similarity   72.5%; Pred. No. 1.3e-75;
Matches 214; Conservative 30; Mismatches 44; Indels 7; Gaps 5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
         |||||:.||||| || :||.::.:.. || :|||:| ||||.:||||||.||.|| |
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         :|| ||||:|||.|:|:::||.| .| .||:||||||:| :| .|||||||||| |
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERDG 118

Qy 116 FVLILEREPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         | :|||.|| |||||||||||||::| ||| ||.|||:|||||||||||||||||||:|:
Db 119 FLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy 176 DLNRGELKLIDFGSGALLKDTVTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
         ||.:|||||||||||| :||||.||||||||||||||||||||||||||.||| ||||||
Db 179 DLRSGELKLIDFGSGAVLKDTVVTDFPDGTRVYSPPEWIRYHRYHGRSAATVWSLGVLLYDM 238

Qy 236 VCGDIPFEHDEEIVKGQYVFRQRVSSECCHLIRWCLSLRPSDRPSFEEIQNHPWM 290
         ||||||||.|||::.|::.|:.|||.|| .||.||||||||:||| ::|..||||
Db 239 VCGDIPFEQDEEILRGRLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWM 293

RESULT 11
PIM3_RAT
ID   PIM3_RAT   STANDARD;   PRT;   326 AA.
AC   O70444;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE   Kid-1) (Kinase induced by depolarization).

GN   Name=Pim3; Synonyms=Kid1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Konietzko U., Kuhl D.;
RT   "Pim-3 is a member of the pim kinase family.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX   MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA   Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA   Bazan N.G., Baudry M., Herschman H.R.;
RT   "KID-1, a protein kinase induced by depolarization in brain.";
RL   J. Biol. Chem. 273:16535-16543(1998).
CC   -!- INDUCTION: By membrane depolarization or forskolin.
CC   -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC   including brain.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.

DR   EMBL; AF086624; AAC68900.1; ALT_INIT; mRNA.
DR   EMBL; AF057026; AAC36065.1; -; mRNA.
DR   HSSP; Q03565; 1HOW.
DR   RGD; 620462; Pim3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_kinase_AS.
DR   InterPro; IPR002290; Ser/Thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
GO   GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
GO   GO; GO:0046777; P:autophosphorylation; IDA.
GO   GO; GO:0016572; P:histone phosphorylation; IDA.
KW   Serine/threonine-protein kinase; Transferase;
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   170   Proton acceptor (By similarity).
FT   BINDING   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 36002 MW; DD6C9BF4635F851E CRC64;

Query Match   67.8%; Score 1131.5; DB 1; Length 326;
Best Local Similarity   72.5%; Pred. No. 1.6e-75;
Matches 214; Conservative 30; Mismatches 44; Indels 7; Gaps 5;

Qy   1 MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
         |||||:.||||| || :||.::.:.. || :|||:| ||||.:||||||.||.|| |
Db   1 MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYAGSR 59

Qy   58 VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
         :|| ||||:|||.|:|:::||.| .| .||:||||||:| :| .|||||||||| |
Db   60 IADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy 116 FVLILEREPEVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
         | :|||.|| |||||||||||||::| ||| ||.|||:|||||||||||||||||||:|:
Db 119 FLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

RESULT 12

Qy   176 DLNRGELKLIIDFGSGGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
           |||||||||| ||||:||||||||||||||||||||||||||||||||||||||:|||||||
Db   179 DLRSGELKLIIDFGSSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   239 VCGDIPFEQDEEILRGRLFFRRRVSPECQOLIEWCLSLRPSERPSLDQIAAHPWM 293

ID   Q4V8M2_RAT   PRELIMINARY;   PRT;   380 AA.
AC   Q4V8M2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC097317; AAH97317.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser_Thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER   1   1
SQ   SEQUENCE   380 AA;   41568 MW;   F82B8B50DD71346 CRC64;

Query Match   67.8%;   Score 1131.5;   DB 2;   Length 380;
Best Local Similarity   72.5%;   Pred. No. 1.9e-75;
Matches 214;   Conservative 30;   Mismatches 44;   Indels 7;   Gaps 5;

Qy   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290

Qy   176 DLNRGELKLIIDFGSGGALLKDTVYTDFPDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDM 235
           |||||||||| ||||:||||||||||||||||||||||||||||||||||||||:|||||||
Db   173 DLRSGELKLIIDFGSGGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDM 232

Qy   116 FVILLEREPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILI 175
           |:|:||||||:|||||||||||||||||||||||||||||||||:|:|||||||||| ||:
Db   114 IADGLPVAVGHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 172

Qy   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   293 VCGDIPFEQDEEILRGRLFFRRRVSPECQOLIEWCLSLRPSERPSLDQIAAHPWM 347

RESULT 13

Qy   1   MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
           ||||||||| |||| |||:|||||:||| |||||:||:||:||||||||||||:|||
Db   1   MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVVYAGSR 59

ID   Q811X8_MOUSE   PRELIMINARY;   PRT;   325 AA.
AC   Q811X8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   KID1.
GN   Name=Pim3; Synonyms=Kid1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu L.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AY026239; AAK16606.1; -; mRNA.
DR   HSSP; Q03656; 1Q99.
SMR;   Q811X8; 36-292.
MGI;   MGI:1355297; Pim3.
GO;   GO:0005524; F:ATP binding; IEA.
GO;   GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO;   GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   325 AA;   35931 MW;   77DEFB8B20F41E3F4 CRC64;

Query Match   67.1%;   Score 1119;   DB 2;   Length 325;
Best Local Similarity   72.2%;   Pred. No. 1.3e-74;
Matches 213;   Conservative 31;   Mismatches 43;   Indels 8;   Gaps 6;

Qy   1   MLLSKINSLAHLRAAP--CNDLHANKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYSGIR 57
           ||||||||| |||| |||:|||||:||| |||||:||:||:||||||||||||:|||
Db   1   MLLSKFGSLAHL-CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVVYAGSR 59

Qy   58   VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSGFSGVIRLLDWFERPDS 115
           || :||||| ||:||:|||||||||||||||||||||| ||||||||:|||||||:||
Db   60   IADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFERPDG 118

Qy   116 FVILLEREPEPVQDLFDFITERGALDEPLARRFFAQVLAAVRHCHINCGVVHRDIKDENILI 175
           |:||||||||:|:||||||||||||:||||||||||:||||||||||||:||||||:|||:
Db   116 FVILLERFPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIII 175

Qy   116 FVILLEREPEPVQDLFDFITERGALDEPLARRFFAQVLAAVRHCHINCGVVHRDIKDENLLV 178
           |:||||||||:|:||||||||||||:||||||||:|:||||||| ||||:|||||||:|:
Db   119 FLLVLEREPPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDENLLV 178

Qy   176 DLNRGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDM 235
          ||| ||||||||||||||||| ||||||||||||||||||||||||||| ||||:|||||
Db   179 DLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHYHGRSATVWSLGVLLYDM 238

Qy   236 VCGDIPFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
          ||||||||:|||| ||:|::|:|||| ||||:|||||||| | ||:|| ||| |||
Db   239 VCGDIPFEQDEEILRGRLFFRRRVSPECCQOLIEWCLSRPSERRSLDKL-CHPWM 292

RESULT 14
Q66I11_XENTR

ID   Q66I11_XENTR PRELIMINARY;   PRT;   318 AA.
AC   Q66I11;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Pim3-prov protein.
GN   Name=pim3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC081340; AAH81340.1; -; mRNA.
DR   SMR; Q66I11; 32-297.
DR   Ensembl; ENSXETG00000009354; Xenopus tropicalis.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkinase_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase;
SQ   SEQUENCE   318 AA;   36547 MW; 48CCF12797F01FDC CRC64;

Query Match   66.6%; Score 1110.5; DB 2; Length 318;
Best Local Similarity   68.8%;
Matches 205; Conservative 40; Mismatches 44; Indels 9; Gaps 4;

Qy   3 LSKINSLAHLRAAPCNDLHANKLAPGKE----KEPLESQYQVGPLLGGSGGFGSVYSGIRV 58
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Db   1 MSSVQVIYHQK--IHNYLNSVFPKDDLPAVKEPFENCYQVGPVIGTGGFGTVYSGVRI 57

Qy   59 ADNLPVAIKHIVEKDRISDWGELNGTRVPMEVVLLKKVSSGFGSGVIRLLDWFERPDSFVL 118
          :|:|:|||||| |: || :| |::|| |:: ::|||:|| |||:|||||||::||| |:
Db   58 SDKLPVAIKHVSRDRIGEMKHM-NGTLVPLEIYLLKKVSNGCRGVIRLLDWYERPDGFII 116

Qy   119 ILERPEPVQDLFDPITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLN 178
          |: |||:||||||||||||||:||||::|| ||:||||||| |.|:|||||||||::||:
Db   117 IMRREPEVQDLFDPITERGALGEELATNFPRQVVEAVRHCHSCDVVHRDIKDENILVDLR 176

Qy   179 RGELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDMVCG 238
          ||||||||||||||| ||| ||||||||||||||| |.||||||:||||| :|||||||
Db   177 TAELKLIDFGSGALLRDAVYTDFDGTRVYSPPEWIRFHXYHGRSATVWSLGILYDMVCG 236

Qy   239 DIPFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWM 290
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Db   237 DIPFEHDDEILKGHKIQYRCRVSRECCQHLIEWCLSKRPSDRPSLEQILAIPWMSGQDNFL 294

RESULT 15
PIM3_XENLA

ID   PIM3_XENLA   STANDARD;   PRT;   323 AA.
AC   Q91822;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN   Name=PIM3; Synonyms=PIM1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RX   MEDLINE=97256766; PubMed=9096695; DOI=10.1074/jbc.272.16.10514;
RA   Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
RA   Aebersold R., Pelech S.L.;
RT   "Identification of the autophosphorylation sites of the Xenopus laevis
RT   Pim-1 proto-oncogene-encoded protein kinase.";
RL   J. Biol. Chem. 272:10514-10521(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC   represent the pim-3 isoform.
CC   -!-
DR   EMBL; L29495; AAA85389.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkinase_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_ATP; FALSE_NEG.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;

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KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN         40    291       Protein kinase.
FT   NP_BIND        46     54       ATP (By similarity).
FT   ACT_SITE      168    168       Proton acceptor (By similarity).
FT   BINDING        69     69       ATP (By similarity).
FT   MOD_RES         4      4       Phosphoserine (By similarity)
FT                                  (partial).
FT   MOD_RES       190    190       Phosphoserine (by autocatalysis).
FT   MOD_RES       205    205       Phosphothreonine (by autocatalysis)
FT                                  (partial).
SQ   SEQUENCE     323 AA;  36964 MW;  AB4DDG1E7A99A38F CRC64;

Query Match            66.1%;
Best Local Similarity  68.6%;
Matches 203;  Conservative 40;  Mismatches 42;  Indels  11;  Gaps  4;

Qy     1  MLLSKINSLAHLRAAPCN-------DLHANKLAPGK-EKEPLESQYQVGPLLGSSGFGSVYS   54
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Db     1  MLLSKFGSLAHI----CNPSNMEHLPVKILQPVKDKEPFEKVYQVGSVVASGGFGTVYS   56

Qy    55  GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPD   114
          |:|| |||| ||||:||:||||||| |||||||| :::||:|||  || ||||||:||||
Db    57  DSRIADGQPVAVKHVAKERVTENGTL-NGVMVPLEIVLLKKVPTAFRGVINLLDWYERPD   115

Qy   115  SFVLILERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENIL   174
          ::|::|||||||||||||||||||||||::||:||||||||||::||||||||||||:|:
Db   116  AFLIVMERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCYNCGVVHRDIKDENLL   175

Qy   175  IDLNRGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYD   234
          :|||||||||||||||||||||||||||||||||||||| ||||||||| |||||||||
Db   176  VDTRNGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWVRYHRYHGRSATVWSLGVLLYD   235

Qy   235  MVCGDIPFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWM      290
          ||:|||||:||||||||||| |::: :|||||||||:||||||||||||: |:||||
Db   236  MVYGDIPFEQDEEIVRRLCFRRRISTECQQLIKWCLSLRPSDRPTLEQIFDHPWM      291
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OM protein - protein search using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: May 4, 2006, 05:25:14 ; Search time 28.6667 Seconds
(without alignments)
902.703 Million cell updates/sec

Title: 1668
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL..........LLPQAASEIHLHSLSPGSSK 313

Scoring table: 1
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BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	2	US-09-237-543-7	Sequence 7, Appl
2	1668	100.0	313	2	US-09-644-450-7	Sequence 7, Appl
3	1584	95.0	313	2	US-09-237-543-8	Sequence 8, Appl
4	1584	95.0	313	2	US-09-644-450-8	Sequence 8, Appl
5	1582	94.8	313	2	US-09-237-543-9	Sequence 9, Appl
6	1582	94.8	313	2	US-09-644-450-9	Sequence 9, Appl
7	1580	94.7	313	1	US-08-463-081B-26	Sequence 26, Appl
8	1580	94.7	313	1	US-08-463-379A-26	Sequence 26, Appl
9	1580	94.7	313	1	US-08-462-390B-26	Sequence 26, Appl
10	1580	94.7	313	1	US-08-462-074B-26	Sequence 26, Appl
11	1580	94.7	313	2	US-08-465-585C-26	Sequence 26, Appl
12	1580	94.7	313	2	US-08-652-446-26	Sequence 26, Appl
13	1355.5	81.3	257	1	US-07-857-224B-41	Sequence 41, Appl
14	1122.5	67.3	455	2	US-09-237-543-5	Sequence 5, Appl
15	1122.5	67.3	455	2	US-09-644-450-5	Sequence 5, Appl
16	1119	67.1	326	2	US-09-237-543-2	Sequence 2, Appl
17	1119	67.1	326	2	US-09-644-450-2	Sequence 2, Appl
18	1113	66.7	323	2	US-09-237-543-6	Sequence 6, Appl
19	1113	66.7	323	2	US-09-644-450-6	Sequence 6, Appl
20	1065.5	63.9	254	2	US-09-237-543-4	Sequence 4, Appl
21	1065.5	63.9	254	2	US-09-644-450-4	Sequence 4, Appl
22	850	51.0	311	2	US-10-184-563-2	Sequence 2, Appl
23	850	51.0	372	2	US-09-949-016-7140	Sequence 7140, Ap
24	379	22.7	1101	2	US-09-770-170-8	Sequence 8, Appl
25	377.5	22.6	776	2	US-09-523-849-34	Sequence 34, Appl
26	373.5	22.4	256	2	US-09-964-956-74	Sequence 74, Appl
27	372	22.3	1356	2	US-09-770-170-6	Sequence 6, Appl
28	371.5	22.3	256	2	US-09-964-956-72	Sequence 72, Appl
29	371	22.2	778	2	US-10-116-326-2	Sequence 2, Appl
30	371	22.2	778	2	US-10-003-690-2	Sequence 2, Appl
31	371	22.2	778	2	US-10-803-277-2	Sequence 2, Appl
32	370	22.2	1323	2	US-09-633-328B-4	Sequence 4, Appl
33	367.5	22.0	512	2	US-09-770-170-2	Sequence 2, Appl
34	367	22.0	281	2	US-09-633-328B-2	Sequence 2, Appl
35	361.5	21.7	630	2	US-09-248-796A-20512	Sequence 20512, A
36	359.5	21.6	631	2	US-10-355-975A-38	Sequence 38, Appl
37	359.5	21.6	631	2	US-10-355-975A-11	Sequence 11, Appl
38	359.5	21.6	668	2	US-09-930-181-2	Sequence 2, Appl
39	349.5	21.0	668	2	US-10-054-579-2	Sequence 2, Appl
40	349.5	21.0	674	2	US-10-283-247-2	Sequence 2, Appl
41	349.5	21.0	674	2	US-10-283-247-7	Sequence 7, Appl
42	345.5	20.7	674	2	US-10-283-247-8	Sequence 8, Appl
43	345.5	20.7	674	2	US-10-817-832B-32	Sequence 32, Appl
44	345	20.7	722	2	US-08-817-832B-32	Sequence 32, Appl
45	344	20.6	722	2	US-09-984-890-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-237-543-7

; Sequence 7, Application US/09237543A
; Patent No. 6143540
; GENERAL INFORMATION:
; APPLICANT: Kapeller, Rosana
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 03580/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-237-543-7

Query Match   100.0%;   Score 1668;   DB 2;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 9e-162;
Matches   313;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGGSGGFGSVYSGIRVAD 60
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Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKIDENILILDLSRG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKIDENILILDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHYGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHYGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECCHLIKWCLSLRPSDRSFEEIIRNHPWWQGDLLPQAAS 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECCHLIKWCLSLRPSDRSFEEIIRNHPWWQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGSSK 313
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RESULT 2
US-09-644-450-7

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;  Sequence 7, Application US/09644450
;  Patent No. 6383791
;  GENERAL INFORMATION:
;  APPLICANT: Kapeller, Rosana
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 035800/175631
;  CURRENT APPLICATION NUMBER: US/09/644,450
;  CURRENT FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 7
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Mus musculus
US-09-644-450-7

Query Match          100.0%;  Score 1668;  DB 2;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 9e-162;
Matches 313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
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Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
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Db  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
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Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300

Qy  301  EIHLHSLSPGSSK  313
         |||||||||||||
Db  301  EIHLHSLSPGSSK  313

RESULT 3
US-09-237-543-8
;  Sequence 8, Application US/0923754A
;  Patent No. 6143540
;  GENERAL INFORMATION:
;  APPLICANT: Kapeller, Rosana
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 035800/175631
;  CURRENT APPLICATION NUMBER: US/09/237,543A
;  CURRENT FILING DATE: 1999-01-26
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 8
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Rattus norvegicus
US-09-237-543-8

Query Match           95.0%;  Score 1584;  DB 2;  Length 313;
Best Local Similarity  94.2%;  Pred. No. 3.4e-153;
Matches 295;  Conservative  8;  Mismatches 10;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||||:||||:|||||||||||||||||||||||||||||:|||||||:||||  :
Db  241  PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy  301  EIHLHSLSPGSSK  313
         |||||||||||
Db  301  EIHLHSLSPSPSK  313

RESULT 4
US-09-644-450-8
;  Sequence 8, Application US/09644450
;  Patent No. 6383791
;  GENERAL INFORMATION:
;  APPLICANT: Kapeller, Rosana
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 035800/175631
;  CURRENT APPLICATION NUMBER: US/09/644,450
;  CURRENT FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 8
;  LENGTH: 313
;  TYPE: PRT
;  ORGANISM: Rattus norvegicus
US-09-644-450-8

Query Match           95.0%;  Score 1584;  DB 2;  Length 313;
Best Local Similarity  94.2%;  Pred. No. 3.4e-153;
Matches 295;  Conservative  8;  Mismatches 10;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
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Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         ||:|||||||||||||||||||||||:|||||||||||||||||||||||||||||||:||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||:||||:|||||||||||||||:||||||||||||||||:|||||||:||||  :
Db  241  PFEHDEEIVKGQVFFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA  300

Qy  301  EIHLHSLSPGSSK  313
         |||||||||  ||
Db  301  EIHLHSLSPSPSK  313

RESULT 5
US-09-237-543-9
;  Sequence 9, Application US/0923754A
;  Patent No. 6143540
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GENERAL INFORMATION:

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;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/237,543A
;   CURRENT FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-237-543-9
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Qy  Query Match         94.8%;  Score 1582;  DB 2;  Length 313;
;   Best Local Similarity   93.9%;  Pred. No. 5.4e-153;
    Matches  294;  Conservative  10;  Mismatches  9;  Indels   0;  Gaps   0;

Qy           1 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 60
               ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db           1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy         121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy         181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDMVCGDI 240
               |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHYHGRSAAVWSLGILLYDMVCGDI 240

Qy         241 PFEHDEEIIKGQVFFRQTVSSECQHLIIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
               ||:|||||||||||||||:|||||||||||:|||||||||||||||||||||:||||||
Db         241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLAIRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy         301 EIHLHSLSPGPSSK 313
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Db         301 EIHLHSLSPGPSK 313
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RESULT 6
US-09-644-450-9

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;   Sequence 9, Application US/09644450
;   Patent No. 6383791
GENERAL INFORMATION:
;   APPLICANT: Kapeller, Rosana
;   TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: 035800/175631
;   CURRENT APPLICATION NUMBER: US/09/644,450
;   CURRENT FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: Patentin Ver. 2.0
;   SEQ ID NO 9
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-644-450-9
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```
Qy  Query Match         94.8%;  Score 1582;  DB 2;  Length 313;
;   Best Local Similarity   93.9%;  Pred. No. 5.4e-153;
    Matches  294;  Conservative  10;  Mismatches  9;  Indels   0;  Gaps   0;

Qy           1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
               ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||:|
Db           1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVSD 60

Qy          61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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RESULT 7
US-08-463-081B-26

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;   Sequence 26, Application US/08463081B
;   Patent No. 5871960 5837487
GENERAL INFORMATION:
;   APPLICANT: Smith, Kendall A. & Beadling, Carol
;   TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
;   TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
;   NUMBER OF SEQUENCES: 35
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
;   STREET: 444 South Flower St. - Suite 1900
;   CITY: Los Angeles
;   STATE: California
;   COUNTRY: USA
;   ZIP: 90071
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0,
;   SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/463,081B
;   FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/104,736
;   FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/796,066
;   FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
;   NAME: Viviana Amzel, Ph. D.
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (213) 622-7700
;   TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 313 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: n.a.
;   TOPOLOGY: n.a.
;   MOLECULE TYPE: peptide
US-08-463-081B-26
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Qy  Query Match         94.7%;  Score 1580;  DB 1;  Length 313;
;   Best Local Similarity   93.9%;  Pred. No. 8.6e-153;
    Matches  294;  Conservative  10;  Mismatches  9;  Indels   0;  Gaps   0;

Qy           1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
               ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||:|
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RESULT 8
US-08-461-379A-26
; Sequence 26, Application US/0461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108; 08/104,736
; APPLICATION NUMBER: & 07/796,066
; FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)470-0700
; TELEFAX: (610)470-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
US-08-461-379A-26
; MOLECULE TYPE: peptide

Qy   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITTERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||| :||
Db   121 ERPEPVQDLFDFITTERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| :
Db   241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGSSK 313
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Db   301 EIHLHSLSPGPSK 313

RESULT 9
US-08-462-390B-26
; Sequence 26, Application US/0462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESSEE: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,390B
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)407-0700
; TELEFAX: (610)407-0701
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: peptide
; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
US-08-462-390B-26
; MOLECULE TYPE: peptide

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db   1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITTERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITTERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGSSK 313
          |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 10
US-08-463-074B-26
Sequence 26, Application US/08463074B
Patent No. 6020155

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Best Local Similarity 93.9%;  Pred. No. 8.6e-153;  Mismatches 9;  Indels 0;  Gaps 0;
Matches 294; Conservative 10;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60
          ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||:|||:||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          |||||||| :||||||| ||||||||:|||:|||||||:|||| :||||||  ||||: :
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
          |||||||||| ||
Db  301 EIHLHSLSPGPSK 313
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GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  (B) STREET: 444 South Flower St. - Suite 1900
  CITY: Los Angeles
  STATE: California
  COUNTRY: USA
  ZIP: 90071
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0,
  SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/463,074B
  FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/104,736
  FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/796,066
  FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph. D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 622-7700
  TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 313 amino acids
  TYPE: peptide
  STRANDEDNESS: n.a.
  TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-463-074B-26

RESULT 11
US-08-465-585C-26
Sequence 26, Application US/08465585C
Patent No. 6029914

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Query Match 94.7%;  Score 1580;  DB 2;  Length 313;
Best Local Similarity 93.9%;  Pred. No. 8.6e-153;
Matches 294; Conservative 10;  Mismatches 9;  Indels 0;  Gaps 0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVAD 60
          ||||||||||||||||   |||||||||||||||||||||||||||||||||||||||:|
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||:|||:||||||||||||||||||||||||||||||:||
Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

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Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGPSK 313
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GENERAL INFORMATION:
APPLICANT: Smith, K. A. & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
  Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
  (B) STREET: 444South Flower St. - Suite 19
  CITY: Los Angeles
  STATE: Californiaa
  COUNTRY: USA
  ZIP: 900071
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/465,585C
  FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: USSN 08/330,108
  FILING DATE: 27-OCT-1994
  APPLICATION NUMBER: USSN 08/104,736
  FILING DATE: 10-AUG-1993
  APPLICATION NUMBER: USSN 07/796,066
  FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph. D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 622-7700
  TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
  LENGTH: 313 amino acids
  TYPE: peptide
  STRANDEDNESS: n.a.

; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-465-585C-26

Query Match   Best Local Similarity 94.7%; Score 1580; DB 2; Length 313;
Matches 294; Conservative 10; Pred. No. 8.6e-153;
                Mismatches 9; Indels 0; Gaps 0;

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Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
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Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

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Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGSSK 313
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RESULT 12
US-08-652-446-26
Sequence 26, Application US/08652446
Patent No. 6057427

GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
                                     (B) STREET: 444 South Flower St. - Suite 1900
  CITY: Los Angeles
  STATE: California
  COUNTRY: USA
  ZIP: 90071
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patentin Release #1.0,
  SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08,652,446
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: EP App. # 96921319.8
  FILING DATE: 8-JAN-1998
  APPLICATION NUMBER: PCT/US/96/09194
  FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/330,108
  FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/463,074
  FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/462,337
  FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/462,390
  FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/465,585
  FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/463,081
  FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/461,379
  FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/739,523
  FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Viviana Amzel, Ph. D.
  REGISTRATION NUMBER: 30,930
  REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 622-7700
  TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 313 amino acids
    TYPE: peptide
    STRANDEDNESS: n.a.
    TOPOLOGY: n.a.
  MOLECULE TYPE: peptide
US-08-652-446-26

Query Match   Best Local Similarity 94.7%; Score 1580; DB 2; Length 313;
Matches 294; Conservative 10; Pred. No. 8.6e-153;
                Mismatches 9; Indels 0; Gaps 0;

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Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |
Db    1 MLLSKINSLAHLRARACNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||   |||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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Db  121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181 EIKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ELKLIDFGSGALLKDTVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQQDLLPQAAS 300
        |:||||||:||||||| |||| ||||||:|||:||||||:|||||:|||||:   ||||
Db  241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGSSK 313
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RESULT 13
US-07-857-224B-41
Sequence 41, Application US/07857224B
Patent No. 5958784

GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Steven A. Benner
  STREET: Hadlaubstrasse 151
  CITY: Zurich
  STATE: none

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;      COUNTRY: Switzerland
;      ZIP: (note: this is an international post code) CH-8092
;      PRIOR APPLICATION DATA: none
;      CLASSIFICATION: 436
;      FILING DATE: 03/25/92
;      APPLICATION NUMBER: US/07/857,224B
CURRENT APPLICATION DATA:
;      SOFTWARE: Microsoft Word
;      OPERATING SYSTEM: Macintosh 7.0
;      COMPUTER: Apple Macintosh
;      MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER READABLE FORM:
;      TELEFAX: (International) 41 1 632 2830
;      TELEPHONE: (International) 41 1 262 2437
TELECOMMUNICATION INFORMATION:
;      TELEX: none
;      TELEFAX: (International) 41 1 632 2830
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
;      LENGTH: 257
;      TYPE: amino acid
;      TOPOLOGY: linear
MOLECULE TYPE:
;      DESCRIPTION: protein
ORIGINAL SOURCE:
;      ORGANISM: rat
FEATURE: Protein kinase; Table 8 Column 46
PUBLICATION INFORMATION:
;      AUTHORS: Hanks, S. K.
;      AUTHORS: Quinn, A. M.
;      AUTHORS: Hunter, T.
;      TITLE: The protein kinase family
;      JOURNAL: Science
;      VOLUME: 241
;      PAGES: 42-52
;      DATE: 1988
US-07-857-224B-41

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Best Local Similarity    98.8%;  Pred. No. 5.2e-130;
Matches  256;  Conservative  0;  Mismatches  0;  Indels  3;  Gaps  2;

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Db   1 SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGE--NGTRVPMEVVLLKK 58

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Db  59 VSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAV 118

Qy 156 RHCHNCGVLHRDIKDENLILIDLSRGEIKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRY 215
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Db 119 RHCHNCGVLHRDIKDENLILIDLSRGEIKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRY 178

Qy 216 HRYHGRSAAVWSLGILLYDMVCGDIPF-EHDEEIIKGQVFRQTVSSECQHLIKWCLSLR 274
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Db 179 HRYHGRSAAVWSLGILLYDMVCGDIPFDEHDEEIIKGQVFRQTVSSECQHLIKWCLSLR 238

Qy 275 PSDRPSFEEIRNHPWMQGD 293
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Db 239 PSDRPSFEEIRNHPWMQGD 257

RESULT 14
US-09-237-543-5
;      Sequence 5, Application US/09237543A
;      Patent No. 6143540
GENERAL INFORMATION:
;      APPLICANT: Kapeller, Rosana
;      TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;      TITLE OF INVENTION: AND USES THEREOF
;      FILE REFERENCE: 035800/175631
;      CURRENT APPLICATION NUMBER: US/09/237,543A
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;      CURRENT FILING DATE: 1999-01-26
;      NUMBER OF SEQ ID NOS: 11
;      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
;      LENGTH: 455
;      TYPE: PRT
;      ORGANISM: Rattus norvegicus
US-09-237-543-5

Query Match              67.3%;  Score 1122.5; DB 2; Length 455;
Best Local Similarity    71.0%;  Pred. No. 7.1e-106;
Matches  213;  Conservative  31;  Mismatches  43;  Indels  13;  Gaps  5;

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Db 130 MLLSKFGSLAHL------CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGGFGTVYA 185

Qy  55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
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Db 186 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 244

Qy 113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAV 155
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Db 245 PDGFLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAV 304

Qy 173 ILIDLSRGEIKLIDFGSGALLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
        :|:|| |||:|||||||||:|||||||||||||||||||||||||||||||:|||||:||
Db 305 LIVDLRSGELKLIIDFGSGAVLKDTVTYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 364

Qy 233 YDMVCGDIPFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
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Db 365 YDMVCGDIPFEQDEEILGRLFPRRVSPECQQIIEWCLSLRPSERPSLDQIAAHPWMLG 424

RESULT 15
US-09-644-450-5
;      Sequence 5, Application US/09644450
;      Patent No. 6383791
GENERAL INFORMATION:
;      APPLICANT: Kapeller, Rosana
;      TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
;      TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
;      CURRENT APPLICATION NUMBER: US/09/644,450
;      CURRENT FILING DATE: 2000-08-23
;      NUMBER OF SEQ ID NOS: 11
;      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
;      LENGTH: 455
;      TYPE: PRT
;      ORGANISM: Rattus norvegicus
US-09-644-450-5

Query Match              67.3%;  Score 1122.5; DB 2; Length 455;
Best Local Similarity    71.0%;  Pred. No. 7.1e-106;
Matches  213;  Conservative  31;  Mismatches  43;  Indels  13;  Gaps  5;
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Search completed: May 4, 2006, 05:27:22
Job time : 29.6667 secs

OM protein - protein search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: May 4, 2006, 05:26:13 ; Search time 92.6667 Seconds
(without alignments)
1411.301 Million cell updates/sec

Title: US-10-705-757-6
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL.........LLPQAASEIHLHSLSPGSSK 313

Scoring table: BLOSUM62
Scoring: Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
      Maximum Match 10%
      Listing first 45 summaries

Database :   Published Applications AA Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	3	US-09-971-791-7	Sequence 7, Appli
2	1668	100.0	313	4	US-10-348-081-14	Sequence 14, Appl
3	1668	100.0	313	4	US-10-664-421-2	Sequence 2, Appli
4	1668	100.0	313	4	US-10-705-757-6	Sequence 6, Appli
5	1668	100.0	313	4	US-10-377-268-10	Sequence 10, Appl
6	1668	100.0	313	5	US-10-941-635-2	Sequence 2, Appli
7	1668	100.0	313	3	US-09-971-791-8	Sequence 8, Appli
8	1584	95.0	313	4	US-10-348-081-12	Sequence 12, Appl
9	1584	95.0	313	4	US-10-705-757-4	Sequence 4, Appli
10	1582	94.8	313	3	US-09-971-791-9	Sequence 9, Appli
11	1582	94.8	313	4	US-10-081-119-18	Sequence 18, Appl
12	1582	94.8	313	4	US-10-394-322A-52	Sequence 52, Appl
13	1582	94.8	313	4	US-10-348-081-13	Sequence 13, Appl
14	1582	94.8	313	4	US-10-664-421-1	Sequence 1, Appl
15	1582	94.8	313	4	US-10-664-421-150	Sequence 150, App
16	1582	94.8	313	4	US-10-705-757-2	Sequence 2, Appli
17	1582	94.8	313	4	US-10-377-268-9	Sequence 9, Appli
18	1582	94.8	313	5	US-10-951-388-18	Sequence 18, Appl
19	1582	94.8	313	5	US-10-951-406-18	Sequence 18, Appl
20	1582	94.8	313	5	US-10-951-477-18	Sequence 18, Appl
21	1582	94.8	313	5	US-10-977-087-18	Sequence 18, Appl
22	1582	94.8	313	5	US-10-941-635-1	Sequence 1, Appli
23	1582	94.8	313	5	US-10-941-635-152	Sequence 152, App
24	1580	94.7	313	4	US-10-620-052A-22	Sequence 22, Appl
25	1315	78.8	253	4	US-10-620-052A-71	Sequence 71, Appl
26	1131	67.8	323	4	US-10-664-421-7	Sequence 7, Appli
27	1131	67.8	323	4	US-10-377-268-15	Sequence 15, Appl
28	1131	67.8	323	5	US-10-941-635-7	Sequence 7, Appli
29	1123.5	67.4	326	4	US-10-348-081-6	Sequence 6, App
30	1123.5	67.4	326	4	US-10-705-757-11	Sequence 11, Appl
31	1123.5	67.4	326	4	US-10-377-268-14	Sequence 14, Appl
32	1123.5	67.4	326	5	US-10-941-635-6	Sequence 6, Appli
33	1122.5	67.3	326	4	US-10-348-081-10	Sequence 10, Appl
34	1122.5	67.3	455	3	US-09-971-791-5	Sequence 5, Appli
35	1122.5	67.3	455	3	US-09-971-791-2	Sequence 2, Appli
36	1119	67.1	326	3	US-09-971-791-2	Sequence 2, Appli
37	1119	67.1	326	4	US-10-348-081-2	Sequence 2, Appli
38	1119	67.1	326	4	US-10-664-421-166	Sequence 166, App
39	1119	67.1	374	4	US-10-618-941-82	Sequence 82, Appl
40	1119	67.1	374	4	US-10-425-114-54264	Sequence 54264, A
41	1119	67.1	326	4	US-10-425-114-54275	Sequence 54275, A
42	1113	66.7	323	3	US-09-971-791-6	Sequence 6, Appli
43	1113	66.7	323	4	US-10-348-081-11	Sequence 11, Appl
44	1113	66.7	323	4	US-10-664-421-8	Sequence 8, Appli
45	1113	66.7	323	4	US-10-377-268-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-971-791-7

; Sequence 7, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/2238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-971-791-7

Query Match   100.0%;   Score 1668;   DB 3;   Length 313;
Best Local Similarity   100.0%;   Pred. No. 8.1e-142;
Matches 313;   Conservative   0;   Mismatches 0;   Indels 0;   Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLLSKINSLAHLRARPCNDLHATKLAAPGKEKEPLESQYQVGPLLGSGSGFGSVYSGIRVAD   60

Qy     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL   120
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Db     61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL   120

Qy    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLSRG   180
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Db    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLSRG   180

Qy    181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 EIKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI   240

Qy    241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS   300

Qy    301 EIHLHSLSPGSSK 313
          |||||||||||||
Db    301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGSSK 313
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RESULT 2
US-10-348-081-14
; Sequence 14, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 14
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-348-081-14

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Query Match             100.0%;  Score 1668;  DB 4;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 8.1e-142;
Matches 313;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGSSK 313
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RESULT 3
US-10-664-421-2
; Sequence 2, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 3.2
;
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-664-421-2

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Query Match             100.0%;  Score 1668;  DB 4;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 8.1e-142;
Matches 313;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
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RESULT 4
US-10-705-757-6
; Sequence 6, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.5281BUS
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-705-757-6

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Query Match             100.0%;  Score 1668;  DB 4;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 8.1e-142;
Matches 313;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
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Db  301 EIHLHSLSPGSSK 313
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Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Db  241  PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241  PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Db  301  EIHLHSLSPGSSK 313
         |||||||||||||
Qy  301  EIHLHSLSPGSSK 313
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RESULT 5
US-10-377-268-10
; Sequence 10, Application US/10377268
; Publication No. US20040171062A1
; GENERAL INFORMATION:
; APPLICANT: HIRTH, KLAUS-PETER
; APPLICANT: MILBURN, MICHAEL VANCE
; TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
; FILE REFERENCE: 039363/0303
; CURRENT APPLICATION NUMBER: US/10/377,268
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: 60/437,929
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/360,651
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-377-268-10

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Query Match    100.0%;  Score 1668;  DB 4;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 8.1e-142;
Matches 313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1  MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy  61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241  PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241  PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301  EIHLHSLSPGSSK 313
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Db 301  EIHLHSLSPGSSK 313
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RESULT 6
US-10-941-635-2
; Sequence 2, Application US/1094163 5
; Publication No. US20050164300A1

; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-941-635-2

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Query Match    100.0%;  Score 1668;  DB 5;  Length 313;
Best Local Similarity  100.0%;  Pred. No. 8.1e-142;
Matches 313;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1  MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy  61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241  PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241  PFEHDEEIIKGQVFRQTVSSECQHLIKWCLSRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301  EIHLHSLSPGSSK 313
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Db 301  EIHLHSLSPGSSK 313
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RESULT 7
US-09-971-791-8
; Sequence 8, Application US/09971791
; Patent No. US20020151204A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle MacBeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 35800/238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-791-8

RESULT 8
US-10-348-081-12

; Sequence 12, Application US/10348081
; Publication No. US20040038246A1
; GENERAL INFORMATION:
; APPLICANT: KORN, Marcus
; APPLICANT: MUELLER, Guenter
; APPLICANT: SCHNEIDER, Rudolf
; APPLICANT: TSCHANK, Georg
; TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
; FILE REFERENCE: DEAV2002/0004 US NP
; CURRENT APPLICATION NUMBER: US/10/348,081
; CURRENT FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 12
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-348-081-12

Query Match   95.0%; Score 1584; DB 3; Length 313;
Best Local Similarity   94.2%; Pred. No. 3e-134;
Matches 295; Conservative   8; Mismatches 10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
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Db   301 EIHLHSLSPSPSK 313

RESULT 9
US-10-705-757-4

; Sequence 4, Application US/10705757
; Publication No. US20040146942A1
; GENERAL INFORMATION:
; APPLICANT: GRUENENTHAL GMBH
; TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
; FILE REFERENCE: 029310.52818US
; CURRENT APPLICATION NUMBER: US/10/705,757
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/EP02/05234
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: DE 101 23 055.9
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-705-757-4

Query Match   95.0%; Score 1584; DB 4; Length 313;
Best Local Similarity   94.2%; Pred. No. 3e-134;
Matches 295; Conservative   8; Mismatches 10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPVMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
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Db   301 EIHLHSLSPSPSK 313

RESULT 10
US-09-971-791-9

; Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
; APPLICANT: Rosanna Kapeller-Libermann
; APPLICANT: Laura A. Rudolph-Owen
; APPLICANT: Kyle Macbeth
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THE
; FILE REFERENCE: 35800/2238856
; CURRENT APPLICATION NUMBER: US/09/971,791
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/644,450
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/237,543

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;   PRIOR FILING DATE: 1999-01-26
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-971-791-9

Query Match     94.8%;  Score 1582;  DB 3;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 4.6e-134;
Matches  294;  Conservative  10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD   60
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Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
         |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         |||||||||||||||||||||||||:||||||||||||||||||||||||||||||:||
Db  121  ERPEPVQDLFDFITERGALQEDLARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||||:|||||||:|||||||||:||||:|||||||:||||:||||||:|||||:
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPGSSK  313
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Db  301  EIHLHSLSPGPSK  313


RESULT 11
US-10-081-119-18
;   Sequence 18, Application US/10081119
;   Publication No. US2003004549191A1
;   GENERAL INFORMATION:
;   APPLICANT: Reinhard, Christoph
;   APPLICANT: Jefferson, Anne B.
;   APPLICANT: Chan, Vivien W.
;   TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;   TITLE OF INVENTION: Target in Cancer
;   FILE REFERENCE: 16932.002
;   CURRENT APPLICATION NUMBER: 2002-02-21
;   PRIOR APPLICATION NUMBER: 60/289,813
;   PRIOR FILING DATE: 2001-02-21
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 18
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-081-119-18

Query Match     94.8%;  Score 1582;  DB 4;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 4.6e-134;
Matches  294;  Conservative  10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD   60
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Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
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Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         |||||||||||||||||||||||||:||||||||||||||||||||||||||||||:||
Db  121  ERPEPVQDLFDFITERGALQEDLARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||||:|||||||:|||||||||:||||:|||||||:||||:||||||:|||||:
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPGSSK  313
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Db  301  EIHLHSLSPGPSK  313


RESULT 12
US-10-394-322A-52
;   Sequence 52, Application US/10394322A
;   Publication No. US20030232391A1
;   GENERAL INFORMATION:
;   APPLICANT: SUNESIS PHARMACEUTICALS, INC.
;   APPLICANT: Prescott, John C.
;   TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
;   FILE REFERENCE: 39750-0006 US
;   CURRENT APPLICATION NUMBER: US/10/394,322A
;   CURRENT FILING DATE: 2003-03-20
;   PRIOR APPLICATION NUMBER: US 60/366,892
;   PRIOR FILING DATE: 2002-03-21
;   NUMBER OF SEQ ID NOS: 70
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 52
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-394-322A-52

Query Match     94.8%;  Score 1582;  DB 4;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 4.6e-134;
Matches  294;  Conservative  10;  Mismatches  9;  Indels  0;  Gaps  0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD   60
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Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVSD   60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL  120
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Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
         |||||||||||||||||||||||||:||||||||||||||||||||||||||||||:||
Db  121  ERPEPVQDLFDFITERGALQEDLARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
         |||||||||:|||||||:|||||||||:||||:|||||||:||||:||||||:|||||:
Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA  300

Qy  301  EIHLHSLSPGSSK  313
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Db  301  EIHLHSLSPGPSK  313


RESULT 13
US-10-348-081-13
;   Sequence 13, Application US/10348081
;   Publication No. US20040038246A1
;   GENERAL INFORMATION:
;   APPLICANT: KORN, Marcus
```

APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2

SEQ ID NO 13
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-348-081-13

RESULT 14
US-10-664-421-1
Sequence 1, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-664-421-1

Query Match   94.8%;   Score 1582;   DB 4;   Length 313;
Best Local Similarity   93.9%;   Pred. No. 4.6e-134;
Matches 294;   Conservative 10;   Mismatches 9;   Indels 0;   Gaps 0;

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Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||:|||||:|||||||||||||||||||||||||||||:||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241  PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
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Db  241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy  301  EIHLHSLSPGSSK 313
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Db  301  EIHLHSLSPGPSK 313
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RESULT 15
US-10-664-421-150
Sequence 150, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 150
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-664-421-150

Query Match   94.8%;   Score 1582;   DB 4;   Length 313;
Best Local Similarity   93.9%;   Pred. No. 4.6e-134;
Matches 294;   Conservative 10;   Mismatches 9;   Indels 0;   Gaps 0;

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Qy    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db    1  MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
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Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
         |||||||||||||||||||||:|||||:|||||||||||||||||||||||||||||:||
Db  121  ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
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Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241  PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
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Db   241  PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
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Db   301  EIHLHSLSPGPSK 313
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OM protein - protein search, using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:27:44 ; Search time 15.3333 Seconds
                                       (without alignments)
                                       944.812 Million cell updates/sec

Title: US-10-705-757-6
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL..........LLPQAASEIHLHSLSPGSSK 313
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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 6: /SIDS5/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
 7: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 8: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep1:*
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12: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	1122.5	67.3	455	9	US-10-784-004-373	Sequence 373, App
2	854.5	51.2	334	8	US-11-096-568A-32575	Sequence 32575, A
3	854.5	51.2	334	9	US-11-087-099-7631	Sequence 7631, Ap
4	850	51.0	311	9	US-10-501-841-32	Sequence 32, Appl
5	850	51.0	311	8	US-10-501-841-40	Sequence 40, Appl
6	379	22.7	504	11	US-11-103-065-2	Sequence 2, Appli
7	378.5	22.7	661	8	US-11-087-099-9816	Sequence 9816, Ap
8	373.5	22.4	661	8	US-10-505-928-690	Sequence 690, App
9	371.5	22.3	256	11	US-10-877-346-74	Sequence 74, Appl
10	371.5	22.3	256	11	US-10-877-346-72	Sequence 72, Appl
11	370	22.2	514	11	US-11-113-424-183	Sequence 183, App
12	362.5	21.7	950	9	US-11-087-099-11500	Sequence 11500, A
13	361	21.6	513	11	US-10-501-035-357	Sequence 357, App
14	359.5	21.6	631	11	US-11-087-099-11726	Sequence 11726, A
15	357	21.4	512	11	US-11-241-056-11	Sequence 11, Appl
16	357	21.4	514	11	US-11-087-099-3612	Sequence 3612, Ap
17	356	21.3	472	11	US-11-087-099-11838	Sequence 11838, A
18	351.5	21.1	504	11	US-11-096-56A-12331	Sequence 12331, A
19	347	20.8	464	11	US-10-501-841-37	Sequence 37, Appl
20	345	20.7	86	9	US-10-784-004-435	Sequence 435, App
21	344	20.6	722	9	US-10-784-004-435	
22	344	20.6	722	9	US-10-784-004-951	Sequence 951, App
23	342.5	20.5	445	11	US-11-096-568A-32575	Sequence 32575, A
24	342	20.5	513	11	US-11-087-099-7631	Sequence 7631, Ap
25	341.5	20.5	619	11	US-11-087-099-12402	Sequence 12402, A
26	338	20.3	1518	11	US-11-087-099-1886	Sequence 1886, Ap
27	336.5	20.2	448	9	US-11-096-568A-18364	Sequence 18364, A
28	334	20.0	651	11	US-10-770-726-67	Sequence 67, Appl
29	334	20.0	651	11	US-11-177-138-10	Sequence 10, Appl
30	333	20.0	620	11	US-11-087-099-3898	Sequence 3898, Ap
31	329	19.7	439	11	US-11-096-568A-20431	Sequence 20431, A
32	329	19.7	439	11	US-11-096-568A-20430	Sequence 20430, A
33	328.5	19.7	443	11	US-11-087-099-905	Sequence 905, App
34	328	19.7	715	9	US-10-204-639-65	Sequence 65, Appl
35	326.5	19.6	689	9	US-10-204-639-17	Sequence 17, Appl
36	326	19.6	473	11	US-11-087-099-8865	Sequence 8865, Ap
37	325.5	19.5	432	11	US-11-096-568A-32576	Sequence 32576, A
38	325.5	19.5	432	11	US-11-087-099-878	Sequence 878, App
39	325	19.5	729	9	US-10-995-561-880	Sequence 880, App
40	325	19.5	737	9	US-10-995-561-876	Sequence 876, App
41	325	19.5	744	9	US-10-995-561-877	Sequence 877, App
42	325	19.5	753	9	US-10-979-095-6	Sequence 6, Appli
43	324.5	19.5	358	9	US-11-087-099-8358	Sequence 8358, Ap
44	324.5	19.5	611	11	US-11-087-099-4237	Sequence 4237, Ap
45	324.5	19.5	706	11	US-11-087-099-4237	

ALIGNMENTS

RESULT 1
US-10-784-004-373
; Sequence 373, Application US/10784004
; Publication No. US20060084066A1
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 373
; LENGTH: 455
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-373

  Query Match   67.3%; Score 1122.5; DB 9; Length 455;
  Best Local Similarity   71.0%; Pred. No.1.9e-90;
  Matches 213; Conservative 31; Mismatches 43; Indels 13; Gaps 5;

Qy   1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
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Db   1 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKVVQYQGAVLGSGGFGTVYA 56

Qy   55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
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Db   57 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 112

Qy   113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHICHNCGVLHRDIKDEN 172
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Db   113 PDGFLIVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 172

Qy   173 ILIDLSRGEIKLLIDFGSGALLKDTVYTPDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
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Db   245 PDGFLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 304

Qy   233 YDMVCGDIPFEHDEEIIKGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
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Db   365 YDMVCGDIPFEQDEEILRGRLFPRRVSPECCQLIEWCLSLRPSERPSLDQIAAHPWMLG 424

RESULT 2

US-10-511-937-2982
Sequence 2982, Application US/10511937
; Publication No. US20060088364A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200010A
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3317
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2982
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2982

Query Match   51.2%;   Score 854.5; DB 8; Length 334;
Best Local Similarity 59.6%;   Pred. No. 3.6e-67;
Matches   164; Conservative   39; Mismatches   67; Indels   5; Gaps   2;

Qy   28 GKKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
            |:|:||::|||||||:||||||||||||:|:.||:||||||::||:|||||||||||||
Db   22 GKDREAFEAEYRLGPLLGKGGFGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy   88 MEVVLLKKVSS---DFSGVIRLLDWFERPDSFVIILERPEPVQDLFDFITERGALQEDLAR 145
            :|:|:||||| :||||||||||||||||:||||||||:|:||||||:||||:||||||
Db   82 LEVALLWKVGAGGGHPGVTIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy   146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVTDFDGTR 205
            ||||||||||||||||||||||||||||||||||||||||||||||||:||:||||||||
Db   142 CFFGQVVAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSSGALLHDEPYTDFDGTR 201

Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQH 265
            |||||||:|||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261

Qy   266 LIKWCLSLRPSDRPSFEEIRNHPWMQ---GDLLPQ 297
            |||||||||||||||||||||||||| ||.||
Db   262 LIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQ 296

RESULT 3
US-10-501-841-32
Sequence 32, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-01440PC

; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; SOFTWARE: Patentin Ver. 124
; SEQ ID NO 32
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-32

Query Match   51.2%;   Score 854.5; DB 9; Length 334;
Best Local Similarity 59.6%;   Pred. No. 3.6e-67;
Matches   164; Conservative   39; Mismatches   67; Indels   5; Gaps   2;

Qy   28 GKKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
            |:|:||::|||||||:||||||||||||:|:.||:||||||::||:|||||||||||||
Db   22 GKDREAFEAEYRLGPLLGKGGFGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP 81

Qy   88 MEVVLLKKVSS---DFSGVIRLLDWFERPDSFVIILERPEPVQDLFDFITERGALQEDLAR 145
            :|:|:||||| :||||||||||||||||:||||||||:|:||||||:||||:||||||
Db   82 LEVALLWKVGAGGGHPGVTIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR 141

Qy   146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVTDFDGTR 205
            ||||||||||||||||||||||||||||||||||||||||||||||||:||:||||||||
Db   142 CFFGQVVAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSSGALLHDEPYTDFDGTR 201

Qy   206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQH 265
            |||||||:|||||||||||||||||||||||||||||||||||:||||||||||||||||
Db   202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCA 261

Qy   266 LIKWCLSLRPSDRPSFEEIRNHPWMQ---GDLLPQ 297
            |||||||||||||||||||||||||| ||.||
Db   262 LIRRCLAPKPSSRPSLEEILLDPWMQTPAEDVTPQ 296

RESULT 4
US-10-501-841-40
Sequence 40, Application US/10501841
; Publication No. US20060084055A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
; TITLE OF INVENTION: and Therapy of Hematological Malignancies
; FILE REFERENCE: 014058-01440PC
; CURRENT APPLICATION NUMBER: US/10/501,841
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 10/057,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: WO PCT/US03/02353
; PRIOR FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-841-40

Query Match   51.0%;   Score 850; DB 9; Length 311;
Best Local Similarity 60.5%;   Pred. No. 8.2e-67;
Matches   161; Conservative   38; Mismatches   65; Indels   2; Gaps   1;

RESULT 5
US-11-103-065-2
; Sequence 2, Application US/11103065
; Publication No. US20050282189A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel E. Lora, Jose M.
; TITLE OF INVENTION: 2150, Human Protein Kinase Family
; TITLE OF INVENTION: Member and Uses Therefor
; FILE REFERENCE: MPI2001-137P1RNM
; CURRENT APPLICATION NUMBER: US/11/103,065
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: US/10/184,563
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,702
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-103-065-2

Query Match   51.0%;   Score 850;   DB 11;   Length 311;
Best Local Similarity   60.5%;
Matches 161;   Conservative 38;   Mismatches 65;   Indels 2;   Gaps 1;

```
Qy   28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP  87
           |::||| ||||||||||||||||||||||||:|:|  :|| .||.:|  |  : |
Db   22 GKDREAFEAEYRLGPLLGKGGFGTVFAGHRLTDRLQVAIKVIPRNRVLGWSPLSDSVTCP  81

Qy   88 MEVVLLKKVSS--DFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
           |:|||| :: |:||  |||||||||:|||| ...| ...||.||:|||||:|||| :
Db   82 LEVALLWKVGAGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPSR  141

Qy  146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTR 205
           |||||||||.|||||:||||||||||||||  .|||||||||||||:|||||:|| |||
Db  142 CFFGQVVAAIQHCSRGVVHRDIKDENLLIDLRRGCAKLIDFGSGALLHDEPYTDFDGTR  201

Qy  206 VYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEIIKGQVFRQTVSSSECQH  265
           |||||||  || :|.  : |||||||||||||||||: |.: .|| || || :|:|||
Db  202 VYSPPEWISRHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHPPAHVSPDCCA 261

Qy  266 LIKWCLSLRPSDRPSFEEIRNHPWMQ 291
           ||:.|| ||||:|||||||||||||
Db  262 LIRRCLAPKPSSRPSLEEILLDPWMQ 287
```

RESULT 6
US-11-087-099-9816
; Sequence 9816, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9816
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
US-11-087-099-9816

Query Match   22.7%;   Score 379;   DB 11;   Length 504;
Best Local Similarity   35.5%;   Pred. No. 2.5e-25;
Matches 94;   Conservative 47;   Mismatches 108;   Indels 16;   Gaps 8;

```
Qy   38 YQVGPLLGSGGGGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
           | :|   | :|  :  : |  .||.|:  :||||||  .||       .:|:   :
Db    8 YKLGKTLGIGSFGKVKIAEHALTGHKVAIKILNRRKIKN---LDMEEKVRREIKILRLFM  64

Qy   98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
           .  ||.: .. :  :   |::   .|  : |  |.|.|.| ||||  |: ||.:|. |
Db   65 HPH--IIRLYEVIETPSDIYVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY  121

Qy  158 CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFPD-GTRVYSPPEWIRYH 216
           || :.||||:| ||:| |  |  .:|:|||     .| .  .    . | :  |||: .
Db  122 CHRNMVVHRDLKPENLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  180

Qy  217 RYHGRSAAVWSLGILLYDMVCGDIPFEHDEII------IKGQVF-FRQTVSSSECQHLKW 269
           . .| .   |  |.:|  :  || |||  ::       .||    :   .|.   .|:
Db  181 LYAGPEVDVWSCGVILLYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS 239

Qy  270 CLSLRPSDRPSFEEIRNHPWMMQGDL 294
           .|.  .. : : ||||.|||:.| |
Db  240 MLVVDPMKRITIPEIRQHPWFQAHL  264
```

RESULT 7
US-10-505-928-690
; Sequence 690, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 690
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-690

Query Match   22.7%;   Score 378.5;   DB 8;   Length 661;
Best Local Similarity   34.6%;   Pred. No. 3.9e-25;
Matches 92;   Conservative 47;   Mismatches 114;   Indels 13;   Gaps 7;

```
Qy   31 KEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEV  90
           |  | ||  : |  |.| |. . : .  :|.|:||| | |..     :      :|::
Db   48 KHNLKHRYELQETIGKGTYGKVRATERFSGRVAIKSIRKDKIKDEQDM---VHIRREI  104

Qy   91 VLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQ 150
           .::   .:: |.:  : :      |::::|   ||.  || ::.  | || |    .||:
Db  105 EIMS--SLNHHIISIYEVFENKDKIVIIMEYASK-GELYDVISERRLSERETRHFFRQ  161

Qy  151 VLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFG-SGALLKDTVYTDFDGTRVYSP 209
           :|.|.||||| |||||| | ||: |  |..    :|   : |   ::     :  |:|:|
```

RESULT 8

US-10-877-346-74
; Sequence 74, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 74
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein kinase
; OTHER INFORMATION: domain Consensus Sequence
US-10-877-346-74

Query Match   22.4%; Score 373.5; DB 9; Length 256;
Best Local Similarity   36.6%; Pred. No. 3.2e-25;
Matches   97; Conservative   45; Mismatches 100; Indels 23; Gaps 10;

```
Qy   38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97

Db  162 IVSAVHYCHKNGVVHRDLKLENILLD-DNCNIKIADFGLSNLYQKDKFLQTFCGSPLYAS 220
Qy  210 PEWIRYHRYHGRSAAVWSLGILLYDMVCGDIP---FEHDEEI--IKGQVFFRQTVSSECQ 264

Db  221 PEIVNGRPYRGPEVDSWALGVLLYTLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDAR 280
Qy  265 HLIKWCLSLRPSDRPSFEEIRNHPWM 290

Db  281 GLIRWMLMVNPDRRATIEDIANHWVV 306
```

RESULT 9

US-10-877-346-72
; Sequence 72, Application US/10877346
; Publication No. US20060014153A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/10/877,346
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/964,956
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 72
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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Qy  157 HCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGGALLKDTVY---TDFDGTRVYSPPEWI 213
Db    1 YELGEKLGSSGAFGKVYKGHKDTGEIVAIKILKKRSLSE----KKKRFLREIQILRLS 55

Qy  214 RYHRYHGRSAAVWSLGILLYDMVCGDIPF---EHDEEI--IKGQVFFR----QTVSSECQ 264
Db   56 --HPNIVRLLGVFEEDDHLYLVMEYMEG-GDLFDYLRNGLLLSEKEAKKIALQILRGLE 112

Qy  265 HLIKWCLSLRPSDRPSFEEIRNHPW 289
Db  113 YLHSRGIVHRDLKPENILLD--ENGTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVL 171

Db  172 EGRGYSSK-VDWWSLGVTLYELLTGKLPFPGIDPLEELFRIKERPRLRLPLPPNCSEELK 230

Db  231 DLIKKCLNKDPEKRPTAKEILNHPW 289
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```
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Serine/Threonine protein kinase Consensus
;   OTHER INFORMATION: Sequence
US-10-877-346-72

Query Match    22.3%;  Score 371.5;  DB 9;  Length 256;
Best Local Similarity  34.5%;  Pred. No. 4.8e-25;
Matches  92;  Conservative  52;  Mismatches  96;  Indels  27;  Gaps  8;

Qy   38  YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
Db    1  YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL----KKKKRERILREIKILKKL-   55

Qy   98  SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH  157
Db   56  -DHPNIVKLYDVFEDDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFYARQILSALEY  113

Qy  158  CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKD---TVYTDFDGTRVSPPEWIRY  215
Db  114  LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL  171

Qy  216  HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQ---------------TVSSE  262
Db  172  GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPPPEWKISPE  228

Qy  263  CQHLIKWCLSLRPSDRPSFEEIRNHPW  289
Db  229  AKDLIKLLIVKDPEKRLTAEEALEHPF  255


RESULT 10
US-11-113-424-183
;   Sequence 183, Application US/11113424
;   Publication No. US20050260713A1
;   GENERAL INFORMATION:
;   APPLICANT: Gangolli et al.
;   TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
;   FILE REFERENCE: 21402-225
;   CURRENT APPLICATION NUMBER: US/11/113,424
;   CURRENT FILING DATE: 2005-04-21
;   PRIOR APPLICATION NUMBER: 60/256,704
;   PRIOR APPLICATION FILING DATE: 2000-12-19
;   PRIOR APPLICATION NUMBER: 60/311,590
;   PRIOR APPLICATION FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: 60/257,314
;   PRIOR APPLICATION FILING DATE: 2000-12-20
;   PRIOR APPLICATION NUMBER: 60/311,613
;   PRIOR APPLICATION FILING DATE: 2001-08-10
;   PRIOR APPLICATION NUMBER: 60/315,617
;   PRIOR APPLICATION FILING DATE: 2001-08-29
;   PRIOR APPLICATION NUMBER: 60/307,506
;   PRIOR APPLICATION FILING DATE: 2001-07-24
;   PRIOR APPLICATION NUMBER: 60/322,358
;   PRIOR APPLICATION FILING DATE: 2001-09-14
;   PRIOR APPLICATION NUMBER: 60/294,075
;   PRIOR APPLICATION FILING DATE: 2001-05-29
;   PRIOR APPLICATION NUMBER: 60/288,153
;   PRIOR APPLICATION FILING DATE: 2001-05-02
;   NUMBER OF SEQ ID NOS: 190
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 183
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: consensus
;   OTHER INFORMATION: sequence
US-11-113-424-183

Query Match    22.3%;  Score 371.5;  DB 11;  Length 256;
Best Local Similarity  34.5%;  Pred. No. 4.8e-25;
Matches  92;  Conservative  52;  Mismatches  96;  Indels  27;  Gaps  8;

Qy   38  YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
Db    1  YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKL----KKKKRERILREIKILKKL-   55

Qy   98  SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH  157
Db   56  -DHPNIVKLYDVFEDDDKLYLVMEYCEG--GDLFDLLKKRGRLSEDEARFYARQILSALEY  113

Qy  158  CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKD---TVYTDFDGTRVSPPEWIRY  215
Db  114  LHSQGIIHRDLKPENILLD-SDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPE-VLL  171

Qy  216  HRYHGRSAAVWSLGILLYDMVCGDIPFEHDEEIIKGQVFFRQ---------------TVSSE  262
Db  172  GKGYGKAVDIWSLGVILYELLTGKPPFPGDDQLL---ALFKKIGKPPPPPPPPPEWKISPE  228

Qy  263  CQHLIKWCLSLRPSDRPSFEEIRNHPW  289
Db  229  AKDLIKLLIVKDPEKRLTAEEALEHPF  255


RESULT 11
US-11-087-099-11500
;   Sequence 11500, Application US/11087099
;   Publication No. US20060041961A1
;   GENERAL INFORMATION:
;   APPLICANT: Abad, Mark S. et al.
;   TITLE OF INVENTION: Genes and Uses for Plant Improvement
;   FILE REFERENCE: 38-21(53450)B EP
;   CURRENT APPLICATION NUMBER: US/11/087,099
;   CURRENT FILING DATE: 2005-03-22
;   SEQ ID NO 11500
;   LENGTH: 514
;   TYPE: PRT
;   ORGANISM: Lycopersicon esculentum
US-11-087-099-11500

Query Match    22.2%;  Score 370;  DB 11;  Length 514;
Best Local Similarity  34.3%;  Pred. No. 1.6e-24;
Matches  91;  Conservative  50;  Mismatches  108;  Indels  16;  Gaps  8;

Qy   38  YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS   97
Db   19  YKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRRKIRN---MDMEEKVRREIKILRLFM   75

Qy   98  SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH  157
Db   76  HPH--IIRLYEVIETPSDIYVVMEYVKS--GELFDYIVEKGRLQEDEARNFFQQIISGVEY  132

Qy  158  CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD--GTRVSPPEWIRYH  216
Db  133  CHRNMVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  191

Qy  217  RYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IKGQVF-FRQTVSSECQHLIKW  269
Db  192  LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSAGARDLIPR  250

Qy  270  CLSLRPSDRPSFEEIRNHPWMQGDL  294
Db  251  MLIVDPMKRMTIPEIRLHPWFQAHL  275


RESULT 12
US-10-501-035-357
;   Sequence 357, Application US/10501035
;   Publication No. US20060046249A1
;   GENERAL INFORMATION:
;   APPLICANT: Bristol-Myers Squibb Company
;   TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
;   TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS
;   TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
;   FILE REFERENCE: D0185 PCT
```

```
;   CURRENT APPLICATION NUMBER: US/10/501,035
;   CURRENT FILING DATE: 2004-07-09
;   PRIOR APPLICATION NUMBER: US 60/350,061
;   PRIOR FILING DATE: 2002-01-18
;   NUMBER OF SEQ ID NOS: 795
;   SOFTWARE: Patentin version 3.2
;
;   SEQ ID NO 357
;   LENGTH: 950
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-501-035-357

  Query Match             21.7%;      Score 362.5; DB 9;   Length 950;
  Best Local Similarity   31.9%;      Pred. No. 1.5e-23;
  Matches    83; Conservative   52; Mismatches  110; Indels  15; Gaps    6;

Qy     38 YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS 97
          |:|| || :  | || ||||||:||||  | || |||| || ||| ||| |||||||||
Db     44 YDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQL----DAVNLEKIYREVQIMKNL- 98

Qy     98 SDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRH 157
          :||: | |||:|||||:||:|||||||||||||||||||||||||:||| :|| | ||:
Db     99 -DHPHIIKLYQVMETKSMLYLVTEYAKN-GEIFDYLANHGRLNESEARRKFWQLSAVDY  156

Qy    158 CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKD-TVYTDFDGTRVYSPPEWIRYH 216
          |||||||||||||||||||||||||||||||||||:| ||| |:||||  |||||| |
Db    157 CHGRKIVHRDLKAENLLLD-NNMNIKIADFGFGNFFKSGELLATWCGSPPYAAPEVFEGQ  215

Qy    217 RYHGRSAAVWSLGILLYDMVCGDIPFEHD------EEIIKGQVFFRQTVSSECQHLIKWC 270
          |||||||||||||||||||||||||||      |:||||| || |||| ||| |:
Db    216 QYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRRRIPYFMSEDCEHLIRRM 275

Qy    271 LSLRPSDRPSFEEIRNHPWM 290
          |:| |||| ||||:
Db    276 LVLDPSKRLTIAQIKEHKWM 295


RESULT 13
US-11-087-099-11726
;   Sequence 11726, Application US/11087099
;   Publication No. US20060041961A1
;   GENERAL INFORMATION:
;   APPLICANT: Abad, Mark S. et al.
;   TITLE OF INVENTION: Genes and Uses for Plant Improvement
;   FILE REFERENCE: 38-21(53450)B EP
;   CURRENT APPLICATION NUMBER: US/11/087,099
;   CURRENT FILING DATE: 2005-03-22
;   NUMBER OF SEQ ID NOS: 12464
;
;   SEQ ID NO 11726
;   LENGTH: 513
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare
US-11-087-099-11726

  Query Match             21.6%;      Score 361; DB 11;   Length 513;
  Best Local Similarity   34.1%;      Pred. No. 9.6e-24;
  Matches    94; Conservative   46; Mismatches  120; Indels  16; Gaps    8;

Qy     28 GKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
          | :    : |:| ||||||||||||||||||||||||| ||||||||||||||||||||
Db      8 GGHSEVLKN-YNLGKTLGLGTFGDVKVAERNVTGQRVAIKILNRRKMETMEMEEKGNR-- 64

Qy     88 MEVVLLKKVSSDF--SGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
          ||||| :|||:|  ||||||||||||||||||| ||:|| |:|:||||||||| | | |
Db     65 --EIKMRLFIDFIHPHIIRVEVIETPKDIFVVMEYCNN-GELLDYIIENGRLQEDEAR    121

Qy    146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GT 204
          | ||||||| ||| ||||||||| |||:|:|:|||||||||||||||||||| ||   |
Db    122 RIFQQILAGVEYCHRIMVVHRDLKPENLLLD-SRYNVKLADFGLSNVMRDGHFLKTSCCS  180

Qy    205 RVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDE------EIIKGQVFFRQT 258
          |||||||| ||||||||||||||||||||||||||| | |       ||||||||||||
Db    181 LNYAAPEIISSKLYAGPEVDVWSCGVVLYALLCGSVPFDDDNIPSLFRKIKGGTYILPSY 240
```

```
Qy    259 VSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
          |||| ||||||||||||||||||| ||||  | ||
Db    241 LSDSARDLIPKLLNIDPMKRITFEEIRVHPWFKNHL 276


RESULT 14
US-11-241-056-11
;   Sequence 11, Application US/11241056
;   Publication No. US20060024807A1
;   GENERAL INFORMATION:
;   APPLICANT: Immunex Corporation
;   APPLICANT: Bird, Timothy A.
;   APPLICANT: Virca, G. Duke
;   APPLICANT: Martin, Unja
;   APPLICANT: Anderson, Dirk M.
;   TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
;   FILE REFERENCE: 2923-US
;   CURRENT APPLICATION NUMBER: US/11/241,056
;   CURRENT FILING DATE: 2005-09-30
;   PRIOR APPLICATION NUMBER: US/09/980,464
;   PRIOR FILING DATE: 2001-11-27
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Patentin version 3.1
;
;   SEQ ID NO 11
;   LENGTH: 631
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-241-056-11

  Query Match             21.6%;      Score 359.5; DB 11;   Length 631;
  Best Local Similarity   31.9%;      Pred. No. 1.7e-23;
  Matches    98; Conservative   54; Mismatches  116; Indels  39; Gaps   10;

Qy      7 NSLAHLRARPCNDLHATKLAPGKEKEP--------LESQYQVGPLLGSGGF 49
          :|:  || |    |||| |          |     || ||||||||||||
Db     17 SALASESARP-----------LADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKTY 68

Qy     50 GSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDW 109
          |||||||||||||||||||  |||||||||||||||||||||||||||::||||||||
Db     69 GKVKKA-RESSGRLVAIKSIRKDKIKDEQDL---LHIREIEIMS--SLNHPHIIAIHEV 122

Qy    110 FERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIK 169
          |||||||||||||||| ||:|||||||| ||| | |:||||||||||| |||||||||:|
Db    123 FENSSKIVIVMEYASR-GDLYDYISERPLSERDARHFFRQIVSALHYCHQNGIVHRDLK 181

Qy    170 DENILIDLSRGEIKLIDFG-SGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSL 228
          |||||||||||||||||| ||||| |||||||||||| ||||||||||||||||||||||
Db    182 LENILLD-ANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL 240

Qy    229 GILLYDMVCGDIPFE-HDEEIKGQV-----FFRQTVSSECQHLIKWCLSLRPSDRPSFEE 283
          ||||||||||||||  | :|||:|      || |||| ||| || ||||||||| ||||
Db    241 GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED 300

Qy    284 IRNHPWM 290
          ||| |||
Db    301 VASHWWV 307


RESULT 15
US-11-087-099-3997
;   Sequence 3997, Application US/11087099
;   Publication No. US20060041961A1
;   GENERAL INFORMATION:
;   APPLICANT: Abad, Mark S. et al.
;   TITLE OF INVENTION: Genes and Uses for Plant Improvement
;   FILE REFERENCE: 38-21(53450)B EP
;   CURRENT APPLICATION NUMBER: US/11/087,099
;   CURRENT FILING DATE: 2005-03-22
;   NUMBER OF SEQ ID NOS: 12464
;
;   SEQ ID NO 3997
;   LENGTH: 512
;   TYPE: PRT
```

; ORGANISM: Solanum tuberosum
US-11-087-099-3997

Query Match   21.4%;   Score 357; DB 11; Length 512;
Best Local Similarity 33.8%;   Pred. No. 2.1e-23;
Matches 91; Conservative 53; Mismatches 101; Indels 24; Gaps 10;

```
Qy      38 YQVGPLLGSSGGGPGGSVYSGGIRVADNL-----PVAIKHVEKDRISDWGELPNGTRVPMEVVLL   93
              |::|:  | |  | :| ||  :|:|  :        | |::|: :  :::::     :|:| ::|:|
Db      19 YKLGKTLGIGSFGKV----KIAEHTLIGHKVAVKILNRRKIRN---MDMEEKVSREIKIL   71

Qy      94 KKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLE  153
              : |||:|  : :|:| |:|||::|:|||:|  :||||| |: |||:::::   :::|::
Db      72 RLFM--HGHISRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIIS  128

Qy     154 AVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPPEW  212
              :|| | ||:||:||:| | || ||:|::||:||  |:| : || :|::|  :|: | | |
Db     129 GVEYCHINMVVHRDLKPENLLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEV  187

Qy     213 IRYHRYHGRSAAVWSLGIILLYDMVCGDIPFEHDEEI------IK-GQVFRQTVSSECQH  265
              |: | : | ||  | || ::| ||:  | ||    |     || |:|: | :  :|: 
Db     188 ISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGYITLPSHLSAGARD  246

Qy     266 LIKWCLSLRPSDRPSFEEIRNHPWMQGDL                                 294
              ||: ||| ||: || | |  |:|:| | |
Db     247 LIPRMLIVDPMKRMTIPEIRLHPWFQAHL                                 275
```

Search completed: May 4, 2006, 05:32:57
Job time : 16.3333 secs

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```
                    GenCore version 5.1.7
            Copyright (c) 1993 - 2006 Bioccceleration Ltd.

OM protein - protein search, using sw model

Run on:            May  4, 2006, 05:12:40 ; Search time 113.667 Seconds
                                            (without alignments)
                                            1209.902 Million cell updates/sec

Title:             US-10-705-757-6
Perfect score:     1668
Sequence:          1 MLLSKINSLAHLRARPCNDL..........LLPQAASEIHLHSPGSSK 313
Scoring table:     BLOSUM62
                   Gapop 10.0 , Gapext 0.5
Searched:          2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:          2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:   Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

Database :  A_Geneseq.21:*
            1: geneseqp1900s:*
            2: geneseqp1908:*
            3: geneseqp2008:*
            4: geneseqp2001s:*
            5: geneseqp2002s:*
            6: geneseqp2003aa:*
            7: geneseqp2003bs:*
            8: geneseqp2004s:*
            9: geneseqp2005s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1668	100.0	313	5	ABG33015	ABG33015 Mouse pro
2	1668	100.0	313	6	AAO19790	AAO19790 Murine PI
3	1668	100.0	313	6	ABR62940	ABR62940 Mouse ser
4	1668	100.0	313	8	ADN97347	ADN97347 Murine Pi
5	1668	100.0	313	8	ADR88371	ADR88371 Mus muscu
6	1668	100.0	313	9	AEA19261	AEA19261 Mouse Pim
7	1668	100.0	313	9	AEB96041	AEB96041 House mou
8	1662	99.6	313	9	AEA19263	AEA19263 Mouse Pim
9	1584	95.0	313	6	AAO19788	AAO19788 Rat PIM1
10	1584	95.0	313	7	ABG33016	ABG33016 Rat prote
11	1584	95.0	313	7	AAO19789	AAO19789 Rat PIM1
12	1584	95.0	313	9	ABR62938	ABR62938 Rat serin
13	1584	94.8	313	9	AEB96039	AEB96039 Norway ra
14	1582	94.8	313	5	ABP54943	ABP54943 Human Pim
15	1582	94.8	313	5	ABG33017	ABG33017 Human pro
16	1582	94.8	313	6	ABU61613	ABU61613 Human PIM
17	1582	94.8	313	7	ABR62939	ABR62939 Human ser
18	1582	94.8	313	7	ADE55368	ADE55368 Human Pro
19	1582	94.8	313	7	ADF45083	ADF45083 Human kin
20	1582	94.8	313	8	ADO19690	ADO19690 Human PRO
21	1582	94.8	313	8	ADR88370	ADR88370 Human PIM
22	1582	94.8	313	8	ADP24227	ADP24227 Human PIM
23	1582	94.8	313	8	ADT07365	ADT07365 Human poly
24	1582	94.8	313	8	ADT14636	ADT14636 human Pim
25	1582	94.8	313	9	ADY86782	Ady86782 Human Pim
26	1582	94.8	313	9	AEA89424	Aea89424 Human Pim
27	1582	94.8	313	9	AEB96037	Aeb96037 Human PIM
28	1580	94.7	313	2	AAW08139	Aaw08139 Human cyt
29	1580	94.7	313	2	AAY87959	Aay87959 Human CR7
30	1580	94.7	313	8	ADI57202	Adi57202 Human PIM
31	1580	94.7	313	8	ADN03170	Adn03170 Human PIM
32	1569	94.1	313	3	ADY85580	Ady85580 Catalytic
33	1355.5	81.3	257	2	AAY43942	Aay43942 Rat prote
34	1315	78.8	253	8	ADI57241	Adi57241 PIM1 domi
35	1215.5	72.9	254	8	ADK71853	Adk71853 Human kin
36	1175	70.4	233	8	ADT07367	Adt07367 Human pro
37	1131	67.8	233	8	ADR88376	Adr88376 Human kin
38	1123.5	67.4	326	8	AAO19792	Aao19792 Murine PI
39	1123.5	67.4	326	7	ABR62933	Abr62933 Mouse pro
40	1123.5	67.4	326	8	ADO60032	Ado60032 CRH signa
41	1123.5	67.4	326	8	ADR88375	Adr88375 Mus muscu
42	1123.5	67.4	326	9	AEB96048	Aeb96048 House mou
43	1122.5	67.3	326	5	AAO20524	Aao20524 Protein s
44	1122.5	67.3	326	6	AAO19791	Aao19791 Rat PIM3
45	1122.5	67.3	326	7	ABR62936	Abr62936 Rat prote

ALIGNMENTS

```
RESULT 1
ID   ABG33015 standard; protein; 313 AA.
AC   ABG33015;
XX
ID   ABG33015 standard; protein; 313 AA.
XX
AC   ABG33015;
XX
DT   20-DEC-2002  (first entry)
XX
DE   Mouse protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; mouse.
OS   Mus musculus.
XX
PN   US200211512120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
XX
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Liebermann R,  Rudolph-Owen LA,  Macbeth K;
XX
DR   WPI; 2002-712471/77.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
PS   Example 3; Page 38-39; 48pp; English.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or
```

RESULT 2

```
CC  differentiative disorders including cancer or haematopoietic neoplastic
CC  disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC  leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC  amino acid sequence of a mouse protein kinase phosphorylation site
XX
SQ  Sequence 313 AA;

Query Match             100.0%;  Score 1668;  DB 5;  Length 313;
Best Local Similarity   100.0%;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||||
Db  301 EIHLHSLSPGSSK 313
```

```
RESULT 2
ID   AA019790 standard; protein; 313 AA.
XX
AC   AA019790;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Murine PIM1 kinase.
XX
KW   Mouse; PIM1 PIM1 kinase; PIM3 kinase; pain; analgesic.
OS   Mus sp.
XX
XX
PN   WO2002093173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; AB269188.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 11; Fig 1F; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
```

RESULT 3

```
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is murine PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1668;  DB 6;  Length 313;
Best Local Similarity   100.0%;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||||
Db  301 EIHLHSLSPGSSK 313
```

```
RESULT 3
ID   ABR62940 standard; protein; 313 AA.
XX
AC   ABR62940;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Mouse serine/threonine protein kinase PIM-1.
XX
KW   Mouse; PIM-1; protein kinase; enzyme.
OS   Mus musculus.
XX
XX
PN   WO2003060130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-00001401.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 40; 40pp; English.
XX
CC   The present sequence is the protein sequence of the murine
CC   serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins
CC   are the paralogues of novel human and murine PIM-3 proteins (see ABR62932
CC
```

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CC   and ABR62933) of the invention, which are therefore expected to be
CC   involved in cancer and cell growth regulation. PIM-3 is also involved in
CC   the development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or type 2
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1668;  DB 7;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 3.8e-158;
Matches 313;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLIAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRARPCNDLHATKLIAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301  EIHLHSLSPGSSK 313
         |||||||||||||
Db  301  EIHLHSLSPGSSK 313

RESULT 4
ADN97347
ID   ADN97347 standard; protein; 313 AA.
XX
AC   ADN97347;
XX
DT   01-JUL-2004 (first entry)
XX
DE   Murine Pim1 SEQ ID NO:6.
XX
KW   mouse; probasin; promoter; transgenic mouse; c-myc; prostate cancer;
KW   Pim1.
XX
OS   Mus musculus.
XX
PN   WO200400010-A2.
XX
PD   31-DEC-2003.
XX
PF   23-JUN-2003; 2003WO-US019818.
XX
PR   21-JUN-2002; 2002US-0390692P.
XX
PA   (REGC) UNIV CALIFORNIA.
XX
PI   Sawyers CL, Ellwood-Yen KB;
XX
DR   WPI; 2004-09050/10.
XX
PT   New transgenic mouse, useful as model system for the study of prostate
PT   cancer and its progression comprising a nucleic acid construct comprising
PT   a promoter operably linked to c-myc gene encoded in prostate cells of
PT   transgenic mouse.
XX
PT   Claim 7; SEQ ID NO 7; 6pp; English.
XX
CC   The invention relates to a novel transgenic mouse whose genome comprises
CC   a nucleic acid construct comprising a promoter having a fully defined
CC   nucleotide sequence comprising 310 bp (ADN97341), where the promoter is
CC   operably linked to c-myc having a fully defined nucleotide sequence
CC   comprising 1320 bp (ADN97342) where the c-myc protein encoded is
CC   expressed in prostate cells of the transgenic mouse at detectable levels.
CC   The transgenic mouse can be used as an in vivo model system for the study
CC   of prostate cancer and its progression. It can also be used in
CC   preclinical and clinical models to test novel diagnostic and therapeutic
CC   modalities including drug therapies relevant to prostate cancer
CC   prevention and progression. The transgenic animal can also be used to
CC   identify molecular markers that can be mediators of progression.
CC   Identification of the mediators is useful since they are potential
CC   therapeutic targets. The present sequence represents murine Pim1.
XX
SQ   Sequence 313 AA;

Query Match             100.0%;  Score 1668;  DB 8;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 3.8e-158;
Matches 313;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1  MLLSKINSLAHLRARPCNDLHATKLIAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLLSKINSLAHLRARPCNDLHATKLIAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD  60

Qy   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLILDLSRG  180

Qy  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy  241  PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301  EIHLHSLSPGSSK 313
         |||||||||||||
Db  301  EIHLHSLSPGSSK 313

RESULT 5
ADR88371
ID   ADR88371 standard; protein; 313 AA.
XX
AC   ADR88371;
XX
DT   18-NOV-2004 (first entry)
XX
DE   Mus musculus PIM 1 protein.
XX
KW   Molecular scaffold; nuclear hormone receptor; TNF receptor;
KW   G-protein coupled receptor; methyl transferase; ligase; PIM; mouse.
XX
OS   Mus musculus.
XX
PN   US2004171062-A1.
XX
PD   02-SEP-2004.
XX
PF   28-FEB-2003; 2003US-00377268.
```

PR   28-FEB-2002; 2002US-0360651P.
PR   16-SEP-2002; 2002US-0411398P.
PR   20-SEP-2002; 2002US-0412341P.
PR   02-JAN-2003; 2003US-0437929P.
XX
PA   (PLEX-) PLEXXIKON INC.
XX
PI   Hirth K, Milburn MV;
XX
DR   WPI; 2004-642017/62.
XX
PS   Disclosure; SEQ ID NO 10; 186pp; English.
XX
PT   Designing a ligand binding to a target molecule, comprises identifying as
PT   molecular scaffolds compounds binding to members of a molecular family,
PT   detecting orientation of scaffolds at a binding site of target, and
PT   synthesizing ligand.
XX
CC   The present invention relates to a method of designing a ligand binding
CC   to a target molecule. The method involves identifying as molecular
CC   scaffolds compounds binding to members of a molecular family, detecting
CC   orientation of scaffolds at a binding site of target, and synthesising
CC   ligand. The invention is useful for designing drug products and for
CC   designing ligand binding to target molecules such as nuclear hormone
CC   receptors, TNF receptors, G-protein coupled receptors, methyl
CC   transferases, ligases, etc. The present sequence is the Mus musculus PIM
CC   1 protein. This sequence is used to illustrate the method of invention.
XX
SQ   Sequence 313 AA;

     Query Match   Best Local Similarity   100.0%;
     Score 1668; DB 8; Length 313;
     Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
     Pred. No. 3.8e-158;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGSSK 313
              |||||||||||||
Db   301 EIHLHSLSPGSSK 313

RESULT 6
ID   AEA19261 standard; protein; 313 AA.
XX
AC   AEA19261;
XX
DT   28-JUL-2005 (first entry)
XX
DE   Mouse Pim-1 protein amino acid sequence - SEQ ID 2.
XX
KW   artery disease; vasotropic; arteriosclerosis; antiarteriosclerotic;
KW   Pim-1.
XX
OS   Mus musculus.

XX
PN   JP2005126413-A.
XX
PD   19-MAY-2005.
XX
PF   19-AUG-2004; 2004JP-00239061.
XX
PR   02-OCT-2003; 2003JP-00344914.
XX
PA   (SOGO-) SOGO IKAGAKU KENKYUSHO KK.
PA   (KATA/) KATAKAMI N.
XX
PI   (SOGO-) SOGO IKAGAKU KENKYUSHO KK.
PI   (KATA/) KATAKAMI N.
XX
DR   WPI; 2005-595567/37.
DR   N-PSDB; AEA19260.
XX
PS   Claim 1; SEQ ID NO 2; 25pp; Japanese.
XX
PT   Therapeutic agent for treating artery disease e.g., arteriosclerosis,
PT   comprises a component which inhibits the function of protein Pim-1.
XX
CC   The invention comprises a therapeutic agent for treating artery disease
CC   which contains a component that inhibits the function of Pim-1 protein.
CC   The therapeutic agent of the invention is useful for the treatment of
CC   arteriosclerosis. The present amino acid sequence represents a mouse Pim-
CC   1 protein of the invention.
XX
SQ   Sequence 313 AA;

     Query Match   Best Local Similarity   100.0%;
     Score 1668; DB 9; Length 313;
     Matches 313; Conservative   0; Mismatches   0; Indels   0; Gaps   0;
     Pred. No. 3.8e-158;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy   301 EIHLHSLSPGSSK 313
              |||||||||||||
Db   301 EIHLHSLSPGSSK 313

RESULT 7
ID   AEB96041 standard; protein; 313 AA.
XX
AC   AEB96041;
XX
DT   20-OCT-2005 (first entry)
XX
DE   House mouse PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS   Homo sapiens.
XX
PN   DE102004004894-A1.

RESULT 8

```
ID   AEA19263 standard; protein; 313 AA.
XX
AC   AEA19263;
XX
DT   28-JUL-2005 (first entry)
XX
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-556609/57.
DR   N-PSDB; AEB96040.
DR   REFSEQ; NP_032868.
XX
PS   Claim 1; Fig 1F; 37pp; German.
XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
     similar use of PIM proteins or nucleic acids.
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (proviral integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the house mouse PIM serine-
CC   threonine kinase protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match       100.0%;  Score 1668;  DB 9;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 3.8e-158;
Matches 313;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||||
Db  301 EIHLHSLSPGSSK 313
```

RESULT 9

```
ID   ABG33016 standard; protein; 313 AA.
XX
AC   ABG33016;
XX
DT   20-DEC-2002 (first entry)
XX
DE   Rat protein kinase phosphorylation site #2.
XX
DE   Mouse Pim-1-related protein amino acid sequence - SEQ ID 4.
XX
KW   artery disease; vasotropic; arteriosclerosis; antiarteriosclerotic;
KW   Pim-1.
XX
OS   Mus musculus.
XX
PN   JP200512641-3-A.
XX
PD   19-MAY-2005.
XX
PF   19-AUG-2004; 2004JP-00239061.
XX
PR   02-OCT-2003; 2003JP-00344914.
XX
PA   (SOGO-) SOGO IKAGAKU KENKYUSHO KK.
PA   (KATA/) KATARAMI N.
XX
PI   KATARAMI N.
XX
PS   Disclosure; SEQ ID NO 4; 25pp; Japanese.
XX
PT   Therapeutic agent for treating artery disease e.g., arteriosclerosis,
PT   comprises a component which inhibits the function of protein Pim-1.
CC   The invention comprises a therapeutic agent for treating artery disease
CC   which contains a component that inhibits the function of Pim-1 protein.
CC   The therapeutic agent of the invention is useful for the treatment of
CC   arteriosclerosis. The present amino acid sequence represents a mouse Pim-
CC   1-related protein of the invention.
XX
DR   WPI; 2005-3595667/37.
DR   N-PSDB; AEA19262.
XX
SQ   Sequence 313 AA;

Query Match       99.6%;  Score 1662;  DB 9;  Length 313;
Best Local Similarity   99.7%;  Pred. No. 1.5e-157;
Matches 312;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLLSKINSLAHLRARPCNDLHATKLAPGCKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIMHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
        |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy  301 EIHLHSLSPGSSK 313
        |||||||||||||
Db  301 EIHLHSLSPGSSK 313
```

KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; rat.
XX
OS   Rattus norvegicus.
XX
PN   US2002115120-A1.
XX
PD   22-AUG-2002.
XX
PF   04-OCT-2001; 2001US-00971791.
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
DR   WPI; 2002-712471/77.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PS   Example 3; Page 39-40; 48pp; English.
XX
PT   Modulating levels or activity of HKID-1 polypeptides, a member of
PT   serine/threonine kinase superfamily, for treating cancer, by contacting
PT   cell expressing the polypeptide with a modulator of the polypeptide.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method is
CC   useful for modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or
CC   differentiative disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a rat protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match   95.0%; Score 1584; DB 5; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||| ||||||| |||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              |||||||||||||||||||||:|||| |||||||||||||||||||||||||||||| ||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
              ||||||||:||||||||:|||||||||:||||||||||||||||||:||||||:| :
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
              |||||||||:|||
Db   301 EIHLHSLSPSPSK 313

ID   AA019789 standard; protein; 313 AA.
XX
AC   AA019789;
XX
DT   11-AUG-2003 (first entry)
XX
DE   Rat PIM1 kinase.
XX
OS   Rattus sp.
XX
KW   Rat; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
PN   WO20029173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; ABZ69187.
XX
PS   Claim 1; Fig 1D; 97pp; German.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is rat PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match   95.0%; Score 1584; DB 6; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||| ||||||| |||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              |||||||||||||||||||||:|||| |||||||||||||||||||||||||||||| ||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
              ||||||||:||||||||:|||||||||:||||||||||||||||||:||||||:| :
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPMMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
              |||||||||:|||
Db   301 EIHLHSLSPSPSK 313

RESULT 11

ABR62938

ID   ABR62938 standard; protein; 313 AA.
XX
AC   ABR62938;
XX
DT   04-DEC-2003 (first entry)
XX
DE   Rat serine/threonine protein kinase PIM-1.
XX
KW   Rat; PIM-1; protein kinase; enzyme.
XX
OS   Rattus norvegicus.
XX
PN   WO200306130-A2.
XX
PD   24-JUL-2003.
XX
PF   20-JAN-2003; 2003WO-EP000492.
XX
PR   19-JAN-2002; 2002EP-00001401.
XX
PA   (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI   Korn M, Mueller G, Schneider R, Tschank G;
XX
DR   WPI; 2003-598536/56.
XX
PT   New human or murine PIM-3 DNAs or polypeptides, useful for as a screening
PT   agent for identifying anti-type 2 diabetes mellitus drugs, or for
PT   treating insulin resistance or type 2 diabetes mellitus.
XX
PS   Example 2; Page 39; 40pp; English.
XX
CC   The present sequence is the protein sequence of the rat serine/threonine
CC   protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the
CC   paralogues of novel human and murine PIM-3 proteins (see ABR62932 and
CC   ABR62933) of the invention, which are therefore expected to be involved
CC   in cancer and cell growth regulation. PIM-3 is also involved in the
CC   development of insulin resistance and type 2 diabetes mellitus. The
CC   invention relates to the use of PIM-3 nucleic acids and proteins in:
CC   screening assays for compounds that modulate insulin resistance or type 2
CC   diabetes mellitus; detection assays for detecting insulin resistance or
CC   type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing,
CC   forensic biology); predictive medicine (e.g. diagnostic or prognostic
CC   assays, monitoring clinical trials, pharmacogenomics); and for the
CC   preparing a medicament for the treatment of insulin resistance or type 2
CC   diabetes mellitus
XX
SQ   Sequence 313 AA;

Query Match   95.0%; Score 1584; DB 7; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |:||||||||||||||||||||||||:|||||||||||||:||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIVKGQVYFRQRVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||:||| :
Db   241 PFEHDEEIKGQVYFRQRQTVSSECQHLIKWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

RESULT 12

AEB96039

ID   AEB96039 standard; protein; 313 AA.
XX
AC   AEB96039;
XX
DT   20-OCT-2005 (first entry)
XX
DE   Norway rat PIM-1 serine-threonine kinase protein.
XX
KW   micturition disorder; urinary dysfunction; uropathic; gene therapy;
KW   PIM-1 protein kinase; serine-threonine kinase; enzyme.
XX
OS   Rattus norvegicus.
XX
PN   DE102004004894-A1.
XX
PD   18-AUG-2005.
XX
PF   30-JAN-2004; 2004DE-10004894.
XX
PR   30-JAN-2004; 2004DE-10004894.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Christoph T;
XX
DR   WPI; 2005-555609/57.
DR   N-PSDB; AEB96038.
DR   REFSEQ; NP_058730.
XX
PT   Identifying substances that regulate PIM kinases, useful for treatment
PT   and diagnosis of urinary incontinence and the urge to urinate, and
PT   similar use of PIM proteins or nucleic acids.
XX
PS   Claim 1; Fig 1D; 37pp; German.
XX
CC   The invention relates to a novel method for identifying substances that
CC   regulate urinary incontinence and the urge to urinate. The method
CC   comprises incubating a test compound with a cell and/or cell preparation
CC   that has synthesized a specific protein of the PIM (provial integration
CC   site) kinase family and measuring either binding of the test compound to
CC   the PIM kinase, or a functional parameter that is altered by the binding.
CC   The method of the invention demonstrates uropathic and gene therapy
CC   applications and may be useful for treatment and diagnosis of urinary
CC   incontinence and the urge to urinate. The method is based upon regulating
CC   the activity or expression of PIM kinases that are involved in bladder
CC   control. The current sequence is that of the Norway rat PIM-1 serine-
CC   threonine kinase protein of the invention.
XX
SQ   Sequence 313 AA;

Query Match   95.0%; Score 1584; DB 9; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Mismatches   10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          ||||||||||||||||||||||||:||:||||||||||||||||||||||||||||:||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   301 EIHLHSLSPGSSK 313
          |||||||||:|||
Db   301 EIHLHSLSPSPSK 313

```
Db
Qy   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIIDLNRG 180
Db
Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
Db
Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
Db
Qy   241 PFEHDEEIIKGQVFFRQTVSSECCQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
Db
Qy   241 PFEHDEEIVKGQVYFRQRVSSECCQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300
Db
Qy   301 EIHLHSLSPGSSK 313
Db
Qy   301 EIHLHSLSPSPSK 313
Db

RESULT 13
ABP54943
ID   ABP54943 standard; protein; 313 AA.
XX
AC   ABP54943;
XX
DT   13-JAN-2003  (first entry)
XX
DE   Human Pim1.
XX
KW   Pim1; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW   mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW   human; gene therapy.
OS   Homo sapiens.
XX
PN   WO200268444-A1.
XX
PD   06-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US005278.
XX
PR   21-FEB-2001; 2001US-0271254P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Reinhard C, Jefferson AB, Chan VW;
XX
PS   Disclosure; Page 80-81; 113pp; English.
XX
CC   The present sequence is the protein sequence of human Pim1, a protein
CC   related to tyrosine threonine kinase (TTK, see ABP54938). TTK
CC   polynucleotides and polypeptides of the invention encompass
CC   polynucleotides and polypeptides having sequence similarity or sequence
CC   identity to human TTK and other genes and gene products related to TTK,
CC   such as Pim1. The invention is based on the finding that TTK is
CC   differentially expressed in various forms of cancer. It provides methods
CC   for the identification of cancerous cells, especially breast cancer and
CC   colon cancer cells, by detection of expression levels of TTK, as well as
CC   diagnostic, prognostic and therapeutic methods. These methods can be used
CC   as the basis of rational therapy. Assays for identifying molecules that
CC   modulate the activity of these genes in cancers, as well as methods of
CC   inhibiting tumour growth by inhibiting the activity of TTK are also
CC   provided
XX
SQ   Sequence 313 AA;

Query Match   94.8%; Score 1582; DB 5; Length 313;
Best Local Similarity   93.9%; Pred. No. 1.6e-149;
   Matches 294; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy     1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGGFGSVYSGIRVAD 60
Db
Qy     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGGFGSVYSGIRVSD 60
Db
Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
Db
Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLKKVSSGFSGVIRLLDWFERPDSFVILL 120
Db
Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
Db
Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCCGDI 240
Db
Qy   241 PFEHDEEIRGQVFFRQVFFRQRVSSECCQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300
Db
Qy   301 EIHLHSLSPGSSK 313
Db

RESULT 14
ABG33017
ID   ABG33017 standard; protein; 313 AA.
XX
AC   ABG33017;
XX
DT   20-DEC-2002  (first entry)
XX
DE   Human protein kinase phosphorylation site.
XX
KW   HKID-1; serine/threonine kinase; cellular proliferative disorder;
KW   differentiative disorder; cancer; haematopoietic neoplastic disorder;
KW   Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML;
KW   Waldenstrom's macroglobulinaemia; WM; human.
OS   Homo sapiens.
XX
PN   US2002115120-A1.
XX
PD   22-AUG-2002.
XX
DR   WPI; 2002-712471/77.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R, Rudolph-Owen LA, Macbeth K;
XX
PS   Example 3; Page 40-41; 48pp; English.
XX
PT   04-OCT-2001; 2001US-00971791.
PR   26-JAN-1999; 99US-00237543.
PR   23-AUG-2000; 2000US-00644450.
XX
CC   The invention describes a method of modulating the level or activity of
CC   human HKID-1 polypeptide, a member of serine/threonine kinase
CC   superfamily. The method involves contacting a cell expressing the
CC   polypeptide or nucleic acid with an agent to modulate the level or
CC   activity of polypeptide, or level of nucleic acid molecule. The method of
CC   modulating the level or activity of HKID-1 polypeptide or
CC   polynucleotide in a subject having or predisposed to having a disorder
CC   involving cancer. Modulating HKID-1 expression or activity is useful for
CC   therapeutic purposes, for treating cellular proliferative and/or
```

```
CC   differentiate disorders including cancer or haematopoietic neoplastic
CC   disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous
CC   leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the
CC   amino acid sequence of a human protein kinase phosphorylation site
XX
SQ   Sequence 313 AA;

Query Match     94.8%;  Score 1582;  DB 5;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 1.6e-149;
Matches  294;  Conservative  10;  Mismatches   9;  Indels   0;  Gaps   0;

Qy          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
              ||||||||||||||||||| :
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy        301 EIHLHSLSPGSSK 313
              ||||||||||||
Db        301 EIHLHSLSPGPSK 313
```

```
CC   PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are
CC   useful for treating chronic pain, particularly of neuropathic or
CC   inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
CC   neurodegenerative diseases). The present sequence is human PIM1 kinase
XX
SQ   Sequence 313 AA;

Query Match     94.8%;  Score 1582;  DB 6;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 1.6e-149;
Matches  294;  Conservative  10;  Mismatches   9;  Indels   0;  Gaps   0;

Qy          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy        181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPMMQGDLLPQAAS 300
              ||||||||||||||||||| :
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPMMQDVLLPQETA 300

Qy        301 EIHLHSLSPGSSK 313
              ||||||||||||
Db        301 EIHLHSLSPGPSK 313
```

Search completed: May 4, 2006, 05:24:46
Job time : 114.667 secs

```
RESULT 15
AA019788
ID   AA019788 standard; protein; 313 AA.
XX
AC   AA019788;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Human PIM1 kinase.
XX
KW   Human; PIM1 kinase; PIM3 kinase; pain; analgesic.
XX
OS   Homo sapiens.
XX
PN   WO2002093173-A2.
XX
PD   21-NOV-2002.
XX
PF   13-MAY-2002; 2002WO-EP005234.
XX
PR   11-MAY-2001; 2001DE-01023055.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Welhe E, Schaefer MK;
XX
DR   WPI; 2003-120715/11.
DR   N-PSDB; ABZ69186.
XX
PT   Method for identifying analgesics, useful particularly for treating
PT   chronic pain, by screening compounds for interaction with PIM-1 or -3
PT   kinase, or related compounds.
XX
PS   Claim 1; Fig 1B; 97pp; German.
XX
CC   The present invention relates to a method of identifying pain-regulating
CC   compounds, involving screening candidate compounds for interaction with
```

OM protein - protein search using sw model

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GenCore version 5.1.7

Run on: May 4, 2006, 05:19:22 ; Search time 20.3333 Seconds
                                        (without alignments)
                                        1481.107 Million cell updates/sec

Title: US-10-705-757-6
Perfect score: 1668
Sequence: 1 MLLSKINSLAHLRARPCNDL.............LLPQAASEIHLHSLSPGSSK 313
Scoring table:

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :   PIR_80:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1668	100.0	313	1	TVMSP1	protein kinase (EC
2	1584	95.0	313	1	S26298	protein kinase (EC
3	1582	94.8	313	1	TVHUP1	protein kinase (EC
4	861.5	51.6	370	1	S55333	protein kinase pim
5	628	37.6	363	2	T22255	hypothetical prote
6	504	30.2	409	2	T15435	hypothetical prote
7	391.5	23.5	481	2	I49072	protein kinase - m
8	379	22.7	504	2	T10449	probable serine/th
9	379	22.7	504	2	S66730	hypothetical prote
10	373	22.4	512	1	JC1446	serine/threonine-s
11	373	22.4	1398	2	T13741	hypothetical prote
12	372	22.3	1358	2	S33653	probable serine/th
13	370	22.2	511	1	A56609	serine/threonine-s
14	367	22.0	512	1	T52633	serine/threonine-s
15	361	21.6	513	1	S60304	serine/threonine-s
16	360.5	21.6	469	2	B84644	probable protein k
17	358.5	21.5	798	2	JC7500	qik protein - chic
18	357	21.4	512	2	T07788	probable serine/th
19	356	21.3	472	2	B90100	SNF1-related kinase
20	353.5	21.2	887	2	T2941	hypothetical prote
21	352	21.1	651	2	S54244	p69Eg3 protein - A
22	351.5	21.1	504	2	T07415	probable serine/th
23	344.5	20.7	414	2	JN0323	Ca2+/calmodulin-de
24	344	20.6	726	2	T13998	hypothetical prote
25	342.5	20.5	445	2	T50802	serine/threonine p
26	342	20.5	502	2	T02306	serine/threonine p
27	342	20.5	513	1	S60303	serine/threonine-s
28	338	20.3	1518	2	S37928	probable protein n
29	334	20.0	746	2	S62365	SNF1-related prote

RESULT 1
TVMSP1

protein kinase (EC 2.7.1.37) pim-1 - mouse

N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene pro
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.;
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Function:
A;Superfamily: kinase-related transforming protein; protein kinase homology <KIN>
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threo
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threon
F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
A;Genetics:
C;Genetics:
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; NID:g
A;Cross-references: UNIPROT:P06803; UNIPARC:UPI00000294AF; GB:M13945; GB:M13946; NID:g

ALIGNMENTS

Query Match   100.0%; Score 1668; DB 1; Length 313;
Best Local Similarity 100.0%; Pred. No. 3.7e-74;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGGGSVSYGIRVAD 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGGGGSVSYGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EIKLIDFGSGALLKDTVYTDFDGTRVVSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFRQVTSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 PFEHDEEIIKGQVFRQVTSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300

Qy 301 EIHLHSLSPGSSK 313
          |||||||||||||
Db 301 EIHLHSLSPGSSK 313

30	332.5	19.9	442	2	T48203	hypothetical prote
31	332	19.9	435	2	E84707	probable protein k
32	330	19.8	461	2	T14822	probable serine/th
33	328.5	19.7	1246	2	G89287	protein H39E23.1 [
34	327.5	19.6	745	2	G01025	serine/threonine p
35	327	19.6	774	2	I48609	probable serine/th
36	326.5	19.6	473	1	T04862	probable serine/th
37	326	19.5	489	2	S59941	serine/threonine-s
38	323.5	19.4	1558	2	T29253	hypothetical prote
39	323	19.4	1192	2	T18611	probable serine/th
40	323	19.4	713	2	S27966	probable serine/th
41	322	19.3	339	2	S56719	serine/threonine-s
42	322	19.3	622	2	S44859	serine/threonine-s
43	322	19.3	423	2	T40224	protein kinase - f
44	321	19.2	552	1	A53621	[hydroxymethylglut
45	321	19.2	552	1	S51025	[hydroxymethylglut

```
Db        301 EIHLHSLSPGSSK 313
              |||||||||||||
```

RESULT 2
S26298

Db   protein kinase (EC 2.7.1.37) pim-1 - rat
     N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
     C;Species: Rattus norvegicus (Norway rat)
     C;Date:25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
     C;Accession: S26298
     R;Wingett, D.; Reeves, R.; Magnuson, N.S.
     A;Title: Characterization of the testes-specific pim-1 transcript in rat.
     A;Nucleic Acids Res. 20, 3183-3189, 1992
     A;Reference number: S26298; MUID:92319652; PMID:1620615
     A;Accession: S26298
     A;Molecule type: mRNA
     A;Residues: 1-313 <WIN>
     A;Cross-references: UNIPROT:P26794; UNIPARC:UPI000013IAD6; EMBL:X63675; NID:g56902; PIDN
     A;Experimental source: testis
     A;Comment: testis-specific transcript is shorter and more stable than the somatic transcri
     C;Comment: Pim-1 autophosphorylates at unknown sites.
     C;Function:
     A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
     C;Note: in testis may be involved in signal transduction events of normal germ cell matu
     C;Superfamily: kinase-related transforming protein; protein kinase homology
     C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
     F;36-290/Domain: protein kinase homology <KIN>
     F;44-52/Region: protein kinase ATP-binding motif
     F;67/Active site: Lys #status predicted

Query Match   95.0%; Score 1584; DB 1; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
           :||||||||||||||:|||||||||:||||||||||||||||||||||||||||||||||:
Db   1 MLLSKINSLAHLRAAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
           ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||:|
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| :
Db   241 PFEHDEEIVKGQVYFRQRVSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy   301 EIHLHSLSPGSSK 313
           |||||||||||||
Db   301 EIHLHSLSPGSSK 313

RESULT 3
TVHUP1

Db   protein kinase (EC 2.7.1.37) pim-1 - human
     N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote
     C;Species: Homo sapiens (man)
     C;Date: 31-Mar-1989 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
     C;Accession: JU0327; A46554; A27476; I58412
     R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
     Gene 90, 303-307, 1990
     A;Title: Primary structure of the putative human oncogene, pim-1.
     A;Reference number: JU0327; MUID:90382681; PMID:2205533
     A;Accession: JU0327
     A;Molecule type: DNA
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Right column:

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     A;Residues: 1-313 <REE>
     A;Cross-references: UNIPROT:P11309; UNIPARC:UPI000000001060; GB:M27903; NID:g189958; PIDN:
     R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
     J, Cell. Biochem. 35, 105-112, 1987
     A;Residues: 1-313 <MEE>
     A;Cross-references: UNIPARC:UPI0000000001060; GB:M24779; NID:g1067790; PIDN:AAA81553.1; PID
     A;Accession: A46554
     A;Reference number: A46554; MUID:88115604; PMID:3429489
     A;Molecule type: mRNA
     A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene relat
     A;Reference number: A46554
     R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
     Gene 54, 105-111, 1987
     A;Title: The cDNA sequence and gene analysis of the human pim oncogene.
     A;Reference number: A27476; MUID:87277423; PMID:3475233
     A;Accession: A27476
     A;Residues: 1-14,'RA',17-313 <ZAK>
     A;Cross-references: UNIPARC:UPI00000149B7C; GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:
     R;Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, A.A.
     Oncogene Res. 1, 103-112, 1987
     A;Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequence and immunolo
     A;Reference number: I58412; MUID:88217305; PMID:3329709
     A;Accession: I58412
     A;Status: preliminary; translated from GB/EMBL/DDBJ
     A;Molecule type: mRNA
     A;Residues: 1-313 <DOM>
     A;Cross-references: UNIPARC:UPI0000000001060; GB:M54915; NID:g189961; PIDN:AAA36447.1; PID:
     C;Comment: Pim-1 autophosphorylates at unknown sites.
     C;Genetics:
     A;Gene: GDB:PIM1
     A;Cross-references: GDB:119495; OMIM:164960
     A;Map position: 6p21.2-6p21.2
     A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
     C;Function:
     A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
     C;Superfamily: kinase-related transforming protein; protein kinase homology
     C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
     F;36-290/Domain: protein kinase homology <KIN>
     F;44-52/Region: protein kinase ATP-binding motif
     F;67/Active site: Lys #status predicted

Query Match             94.8%;  Score 1582;  DB 1;  Length 313;
Best Local Similarity   93.9%;
Matches 294;  Conservative 10;  Mismatches 9;  Indels 0;  Gaps 0;

Qy     1 MLLSKINSLAHLRARPCNDLHATKLAPGKGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
           :||||||||||||||:|||||||||:|||||||||||||||||||||||||||||||:||:
Db     1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy   121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
           |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db   121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
           ||||||||:||||||||:||||||||:||||||||||||||||||:|||||||:||||| :
Db   241 PFEHDEEIRGQVFFRQRVSSECQHLIRWCLAIRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGSSK 313
           |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 4
S55333

Db   protein kinase pim-2 (EC 2.7.1.-) - mouse
```

C;Species: Mus musculus (house mouse)
C;Date: 10-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 proto-oncogene 1
A;Reference number: S55333
A;Accession: S55333
A;Molecule type: mRNA
A;Residues: 1-370 <VAN>
A;Cross-references: UNIPROT: Q62070; UNIPARC: UPI0000028629; GB:L41495; NID:g9765065; PIDN:
A;Accession: A43093
A;Note: 40K form
A;Molecule type: mRNA
A;Residues: 'M, 27-370 <VA2>
A;Cross-references: UNIPARC:UPI00000278BE; GB:L41495; NID:g9765065; PID:
A;Note: 37K form
A;Accession: B43093
A;Molecule type: mRNA
A;Residues: 'M, 61-370 <VA3>
A;Cross-references: UNIPARC:UPI00000278BF; GB:L41495; NID:g9765065; PIDN:AAA98924.1; PID:
A;Note: 34K form
C;Comment: Pim-2 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted

Query Match   51.6%;   Score 861.5;   DB 1;   Length 370;
Best Local Similarity   55.7%;   Pred. No. 3.4e-35;
Matches 167;   Conservative 41;   Mismatches 87;   Indels 5;   Gaps 2;

```
Qy     12 LRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEK 71
              ||||| |: |||   | :   | :||||||||||| ||||||||| |  |||||:| :
Db     65 LQGHPSPPVTPQPPGGKDRAAFEAEYLGLPLLGKGGFGTVFAGHRVTDRRQVAIKVISR 124

Qy     72 DRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFERDSFVLILERPEPVQDL 129
              |: :| |||  ||  | ||||||||   | | : ||||||||||| |:| ||||||||
Db    125 NRVLGWSTVSDSVTCPLEVALLWKVGEGNGHPGVIRLLDWFETPEGFMLVLERMPAQDL 184

Qy    130 FDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGS 189
              |||||| | |||||||||||||||| |  | |||||||||||||||  ||| ||||||
Db    185 FDYITEKGPLGESCSRSFTQVVAAVQHCHARGVVHRDIKDENILIDLCRGSIKLIDFGS 244

Qy    190 GALLKDTVYTFDPGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEII 249
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ::
Db    245 GALLHDEPYTDFDGTRVYSPPEWISRHQYHALPATVWSLGVLLYDMVCGDIPFERDQEIL 304

Qy    250 KGQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAASEIILHSLSP 309
              ||||||||||||||||||| ||| ||||||||||||||||||||| || ::|||||||:
Db    305 EAELHFPAHVSPDCCALIRRCLAPKPCSRPSLEEILLDPWMQS---PABEKPINSSKGSP 361
```

A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; UNIPARC:UPI0001755A4; EMBL:Z34800; PIDN:CAA84323.
C;Genetics:
A;Experimental source: clone F45H7
C;Genetics:
A;Gene: CESP:F45H7.4
A;Map position: 3
A;Introns: 72/3; 160/3; 310/1

Query Match   37.6%;   Score 628;   DB 2;   Length 363;
Best Local Similarity   46.0%;   Pred. No. 6.2e-24;
Matches 122;   Conservative 48;   Mismatches 89;   Indels 6;   Gaps 3;

```
Qy     35 ESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLK 94
             :||| |||| |||| ||||||||||||||||:   |  ||:|||||||||| |:||:|
Db     28 KKNYKLKAELGRGGFGTVYRAVRTCDNALVAVKFIERSNVKEWARI-NGEQVPMEICMLA 86

Qy     95 KVSSDFSGVIRLLDWFERDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEA 154
             :: : | |||||||||| :|| : ||  ||||||||||:||| |:|||||||| :||:
Db     87 KCSK-VRGVIRLLDWYSIPEGFLIVWMERPYPCIDMPDFIKGQGKISEDMARFLFRQIAVT 145

Qy    155 VRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTFDPGTRVYSPPEWIR 214
             ||||  |||||||||||| | | |   ||||||||||||||||||||||||||||||:
Db    146 VHECVQNRVLHRDLKDENIVIDLVTGSTKLIDFGAATVLRRSQYSDFQGTRLYCPEWFL 205

Qy    215 YHRYHGRSAAVWSLGILLYDMVCGDIPFEHDEII----IKGQVFRQTVSSECQHLIKWC 270
             ||||||||||||||| || |:||||||||||| |     ||||||| ||||||||||||
Db    206 HSLYLGREAAVWSLGVLYNSLANGRLPFRNEKDICTAHLLGPLPFFVPVSAAEVKDLISKC 265

Qy    271 LSLRPSDRPSFEEIRNHPWMQGDLL 295
             || |:||||||||||||||||||||
Db    266 LTFDFPQRCSLEAILNHPWKQQTL 290
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RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15435
R;Favello, A.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid C06E8.
A;Reference number: Z18350
A;Accession: T15435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-409 <FAV>
A;Cross-references: UNIPARC:UPI000017B744; EMBL:U00034; NID:g458983; PID:g458986; PIDN
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C06E8.3
A;Introns: 24/1; 76/3; 107/2; 145/3; 199/1; 307/1; 375/1

Query Match   30.2%;   Score 504;   DB 2;   Length 409;
Best Local Similarity   36.9%;   Pred. No. 6.5e-18;
Matches 109;   Conservative 54;   Mismatches 124;   Indels 8;   Gaps 5;

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Qy      1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
             |: :| :|  ||| ||||||||||||||||     :::| ||  |||||:||||||||||
Db      1 MIKRKLQDLAVCCSYQVDFLHEKK----HSVKEFKRKYEVLDEIGRGGFGIVYEATTRQD 56

Qy     61 -NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERDSFVLI 119
              ||||||||:||||:|||||||||||||:|||:|||||:: : | |||||||||||| :
Db     57 GQQPVAVKFVQHKVHRSW-TMTCRQLIPSEVCHL-ETCEDIPGVIKILDWFANSKGFLIV 114

Qy    120 LEREPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHN-CGVLHRDIKDENILIDLS 178
             || ||:|||||||||||||||||||||||||||||| ||| |||||||||||| | |:
Db    115 MERPANCMDLFDMVSVHGPLNEDMGKFIFKQVITTVFNMYSKHGLLHRDIKDENIIVNMN 174

Qy    179 RGEIKLIDFGSGALLKDTVYTFDPGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG 238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    175 TGEVKLVDFGATAYABKATKKEFQGTRSYCPPEWPRDQLYLPLEATSWSLGVLFLILTG 234
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Qy  239  DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGD  293
              :::|::||||||||||||||||||||||||||||||||||||||
Db  235  KLPFRNEIQICLGNVKFPPDLSKEVCQLVKSCLTTSTSARASLAQIAAHPWMETD  289
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RESULT 7
I49072
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I49072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
A;Title: Identification of novel protein kinases expressed in the myocardium of the deve
Mech. Dev. 48, 153-164, 1994
A;Reference number: I49071; MUID:95200798; PMID:7893599
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-481 <RES>
A;Cross-references: UNIPARC:UPI000017A422; EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PI
A;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif

Query Match   23.5%; Score 391.5; DB 2; Length 481;
Best Local Similarity 33.5%;
Matches 104; Conservative 55; Mismatches 126; Indels 25; Gaps 11;

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Qy    4  SKINSLAHLRARP-----CNDLHATKLAPGEKEPLE-SQYQVGPLLGSGGFGSV-YSGI  56
Db   33  SRVGSRRAAEVRPEAMVIMSEFRAVPSGTGRSQKPLRVGFYDVERTLGKGNFAVVKLRGH  92

Qy   57  RVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSF 116
Db   93  RVT-KTQVAIKILDKTRL----DSSNLEKIYREVQLMKLL--NHPNIIKLYQVMETKDML 145

Qy  117  VLILERPEPVQDLLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILID 176
Db  146  YIVTEFAKN-GEMFDYLTSNGHLSENEARQKFWQILSAVEYCHNHHIVHRDLKTENLLLD  204

Qy  177  LSRGEIKLIDFGSGALLK-DTVYTDFDGTRVSPPEWIRYHRYHGRSAAVWSLGILLYDM  235
Db  205  -SNMDIKLADFGFGCNFYKPGEPLSTCVGSPPYAAPEVFEGKEYEGPQLDVWSLGVVLVYL 263

Qy  236  VCGDIPFEHD-------EEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPW 289
Db  264  VCGSLPFDGPNLPTLRQRVLEGRFRIPFFMSQDCETLIRRMLVVDPAKRITIAQIRQHRW  323

Qy  290  MQGSD--LLPQ 297
Db  324  MQADPTLLQQ  333
```

RESULT 8
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17020
A;Accession: T10449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; UNIPARC:UPI00000A4B92; EMBL:Y10036
A;Keywords: ATP
A;Experimental source: cv. Masterpiece; cotyledon
A;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match   22.7%; Score 379; DB 2; Length 504;
Best Local Similarity 35.5%; Pred. No. 8.3e-12; Indels 16; Gaps 8;
Matches 94; Conservative 47; Mismatches 108;

```
Qy   38  YQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVS  97
Db    8  YKLGKTLGISGSFGKVKIAEHALTGHKVAIKILNRKIKH---LDMEEKVRREIKILRLFM  64

Qy   98  SDFSGVIRLLDWFERPDSFVLILERPEPVQDLLFDFITERGALQEDLARGFFWQVLEAVRH 157
Db   65  HPH--IIRLYEVIETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQIISGVEY  121

Qy  158  CHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPPEWIRYH  216
Db  122  CHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAPEVISGK  180

Qy  217  RYHGRSAAVWSLGILLYDMWVCGD-IPFEHDEEI------IKGQVF-FRQTVSSECQHLIKW 269
Db  181  LYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSGARELIPS  239

Qy  270  CLSLRPSDRPSFEEIRNHPWMMQGDL 294
Db  240  MLVVDPMKRITIPEIRQHPWFQAHL  264
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RESULT 9
S66730
hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Oct-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiemann, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Molecule type: DNA
A;Accession: S66730
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT:Q08217; UNIPARC:UPI000012DF35; EMBL:Z74788; NID:g1419846; PI
A;Experimental source: strain S288C
A;Genetics:
A;Cross-references: SGD:S0005405
A;Map position: 15L
A;Keywords: ATP
F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif

Query Match   22.7%; Score 379; DB 2; Length 1101;
Best Local Similarity 33.5%; Pred. No. 1.6e-11; Indels 26; Gaps 8;
Matches 91; Conservative 60; Mismatches 95;

```
Qy   36  SQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRI--SDW-----GELPNGTRVP  87
Db  839  SDFTILQVMGEGAYGKVNLCIHNREHYIVIKMIFKERILVDTWVRDRKLGTIPSEIQI-  897

Qy   88  MEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQ------DLFDFITERGALQE 141
Db  898  --MATLNKNSQE--NILKLLDFFEDDDYYI----ETPVHGETGSIDLFDVIEFKDMVE  949

Qy  142  DLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDF 201
Db  950  HEAKLVFKQVVASIKHLHDQGIVHRDIKDENIVD-SHGFVKLIDFGSAAYIKSGPFDVF 1008

Qy  202  DGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMWVCGDIPFEHDEEIIKGQVFFRQT-V 259
Db 1009  VGTMDYAAPEVLGGSSYKGKPQDIWALGVLLYTIIYKENPYYNIDEILEGELRFDKSEHV 1068

Qy  260  SSECQHLIKWCLSLRPSDRPSFEEIRNHPWMMQ 291
Db 1069  SEECISLIKRILTREVDKRPTIDELYEDKWLK 1100
```

RESULT 10
JC1446
N;Alternate names: protein kinase SNF1 homolog
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Oct-2004
C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number:
A;Accession: JC1446; MUID:93013041; PMID:1339373
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; UNIPARC:UPI000012DE43; GB:M93023; NID:g166599; PIDN:
R;Thuemler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A;Reference number: S58266
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: UNIPARC:UPI00000SDEE0; EMBL:X86966; NID:g9288909; PIDN:CAA60529.1; PI
R;Thuemler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes i
A;Reference number: S66314; MUID:96122233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: UNIPARC:UPI00000SDEE0; EMBL:X86966; NID:g9288909; PIDN:CAA60529.1; PI
C;Genetics:
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
A;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match   22.4%;   Score 373;   DB 1;   Length 512;
Best Local Similarity   34.7%;   Pred. No. 1.6e-11;
Matches   94;   Conservative   47;   Mismatches   114;   Indels   16;   Gaps   8;

```
Qy  32 EPLESQYQVGPLLGSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV  91
        :||| |||||||  || |: |  :||| |:|: |||   :  :.:  |  :  :
Db  13 ESILPNYKLGRTLGIGSFGRVKIAEHALTGHKVAVKILNRRKIKN--MEMEEKVRREIK  69

Qy  92 LKKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQV 151
        :  ||| :||     :|||::. || ::||::: :| | ::||::||:|:|||:: |:||
Db  70 IIRLFMHPH--IIRLYEVIETPFDIYLVMEYVNS-GELFDYIVEKGRLQEDEARNFFQQI 126

Qy 152 LEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GTRVYSPP 210
        ::||::||:.||:|||:|:|||:||  :  ||:|||| ||:||||||| | |:||| |:
Db 127 ISGVEYCHRNMVVHRDLKPENLLLD-SKCNVKIADFGLSNIMRDGHFLKTSCGSPNYAAP 185

Qy 211 EWIRYRYHYHGRSAAVWSLGILLYDMVCGDIPFEHDEEI------IKGQVF-FRQTVSSEC 263
        | :   :::.| .::||| |:::| : ||:|||   |::      ||| ::  : |.|
Db 186 EVISGKLYAGPEVDVWSCGVILLYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSPGA 244

Qy 264 QHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
         .|:: :|| .| :|| : ||| |||:| .|
Db 245 RDLIPRMLVVDPMKRVTIPEIRQHPWFQAHL 275
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RESULT 11

T13741
N;Alternate names: protein 2285.8 - fruit fly (Drosophila melanogaster)
hypothetical protein 2285.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
R;Reference number: 217668
A;Accession: T13741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1398 <MUR>
A;Cross-references: UNIPROT:O77268; UNIPARC:UPI0000820A3; EMBL:AL031765; NID:e1371523
C;Genetics:
A;Cross-references: FlyBase:FBgn0006667
A;Note: EG:2285.8

Query Match   22.4%;   Score 373;   DB 2;   Length 1398;
Best Local Similarity   32.6%;   Pred. No. 3.8e-11;
Matches   90;   Conservative   59;   Mismatches   109;   Indels   18;   Gaps   9;

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Qy  29 KEKEPLE-SQYQVGPLLGSGGFGSV-YSGIRVADNLPVAIKHVEKDRISDWGELPNGTRV  86
Db 131 KLKEPMRVGFYDIERTIGKGNFAVVKLARRRITKN-EVAIKIIDKSQL---DQTNLQKV 185

Qy  87 PMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLARG 146
Db 186 YREVEIMKRLKHPH--IIKLYQVMETKNMYIYVSEYASQ-GEIFDYIAKYGRMSESAARF 242

Qy 147 FFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFG-SGALLKDTVYTDFGDGTR 205
Db 243 KFWQIISAVEYCHKKGIVHRDLKAENLLLDLNM-NIKIADFGFSNHFKPGELLATWCGSP 301

Qy 206 VYSPPEWIRYRYHYHGRSAAVWSLGILLYDMVCGDIPFEHD-----EEIKGQVFFRQTV 259
Db 302 PYAAPEVFEGKQYTGPEIDIWSLGVVLYVLVCGALPFDGSTLQSLRDRVLSGRFRIPFFM 361

Qy 260 SSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLL 295
Db 362 SSECHLIRRMLVLEPTRRYTIDQIKRHRWMCPELL 397
```

RESULT 12

S33653
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisia
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 02-Aug-1994 #text_change 05-Oct-2004
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kab
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae en
A;Reference number: S33653
A;Accession: S33653; S36717; S36732; MUID:93311122; PMID:8322517
A;Molecule type: nucleic acid sequence not shown
A;Accession: S33653
A;Status:
R;Ouellette, F.; Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.;
submitted to the EMBL Data Library, January 1993
A;Description: Sequencing of Chromosome I from Saccharomyces cerevisiae: analysis of a
A;Reference number: S36711
A;Accession: S36717
A;Molecule type: DNA
A;Residues: 1-1358 <CLA>
A;Cross-references: UNIPROT:P31374; UNIPARC:UPI000017A449; EMBL:L05146; NID:g171851; PIDN:AAC04940.1;
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey,
Yeast 8, 133-145, 1992
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptio
A;Reference number: S22266; MUID:92221690; PMID:1561836
A;Accession: S36732

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-862 <CL2>
A;Cross-references: UNIPARC:UPI000017A44A; EMBL:S93805
R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P.
Gene 107, 111-118, 1991
A;Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Saccharomy
A;Reference number: JH0483; MUID:92077420; PMID:1743509
A;Accession: JH0486
A;Molecule type: DNA
A;Residues: 1-72, 'E', 74-154 <SID>
A;Cross-references: UNIPARC:UPI000017A44B
A;Genetics:
A;Cross-references: UNIPARC:UPI000017A44B
A;Gene: SGD:FUN31; SSP138; MIPS:YAL017w
A;Map position: 1L
A;Cross-references: SGD:S0000015; MIPS:YAL017w
A;Gene: SGD:FUN31;
C;Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specific protein kin
F;1104-1112/Region: protein kinase ATP-binding motif
F;1104-1112/Domain: protein kinase homology <KIN>
F;8,128/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;1232/Active site: Asp #status predicted

Query Match
Best Local Similarity 22.3%; Score 372; DB 2; Length 1358;
Matches 88; Conservative 54; Pred. No. 4.2e-11; Mismatches 100; Indels 16; Gaps 6;

```
Qy    44 LGSGGFPGSVYSGIRVADNLPVAIKHVEKDRI--SDWGELPNGTRVPMEVVLLKKVS-SDF 100
            ||:|||
Db  1104 MGEGAYGKVNLCIHKKNRIVIVIKMIFKERILVDTWTWRDRKLGTIPSEIQIMATLNKKPH 1163

Qy   101 SGVIRLLDWFERPDSFVLILEREPEVQ-----DLFDFITERGALQEDLARGFFWQVLEA 154
Db  1164 ENIRLLDFFEDDYYYI---ETPVHGETGCIDLFDLIEFKTNMTEFEAKLIFKQVVAG 1219

Qy   155 VRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVYTDFDGTRVYSPPEWIR 214
Db  1220 IKILHDQIVHRDIKDENVIVD-SKGFVKIIDFGSSAAYKSGPFDVFVGTIDYAAPEVLG 1278

Qy   215 YHRYRHGRSAAVWSLGILLLYDMVCGDIPFEHDEEIIKGQVFFR--QTVSSECQHLIKWCLS 272
Db  1279 GNPYEGQOPQDIWAIGILLYTVVFKENPFYNIDEILEGDLKFNNAEEVSEDCIELIKSILN 1338

Qy   273 LRPSDRPSFEEIRNHPWM 290
Db  1339 RCVPXKRPTIDDINNDKWL 1356
```

Best Local Similarity 33.8%; Pred. No. 2.3e-11;
Matches 93; Conservative 49; Mismatches 117; Indels 16; Gaps 8;

```
Qy    28 GKEKEPLESQYQVGPLLGSGGFPGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
Db     9 GSSVESFLRNYKLGKTLGSGGFPGKVKIAEHTLTGHKVAVKILNRRKIKN--MEMEKVR 65

Qy    88 MEVVLLKKVSSDFSGVIRLLDWFERPDSFVLILEREPEVQDLFDFITERGALQEDLARGF 147
Db    66 REIKILRLFMHPH--IIRLYEVETPSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARKF 122

Qy   148 FWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVYTDFD-GTRV 206
Db   123 FQQIISGVEYCHRNMVVHRDLKPENLLD-SKWNVKIADFGLSNIMRDGHFLKTSCGSPN 181

Qy   207 YSPPEWIRYHRYRHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------IK-GQVFFRQTV 259
Db   182 YAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGMISLPSHL 240

Qy   260 SSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
Db   241 SAGARDLIPRMLIVDPMKRMTIPEIRMHPWFQAHL 275
```

RESULT 13
A56009
serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 05-Oct-2004
C;Accession: A56009
R;Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cer
tase of Saccharomyces cerevisiae.
A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; UNIPARC:UPI00000AAD0C; GB:D26602; NID:g496384; PIDN:
C;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match
Best Local Similarity 22.2%; Score 370; DB 1; Length 511;

RESULT 14
T52633
serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis t
N;Alternate names: SNF1 protein kinase omolog AKIN11
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 05-Oct-2004
C;Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein ki
A;Reference number: Z25116; MUID:99238528; PMID:10220464
A;Accession: T52633
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
A;Cross-references: UNIPROT:P92958; UNIPARC:UPI00000AC16D; EMBL:X99279; PIDN:CAA67671.1
C;Function:
A;Description: EC 2.7.1.-; serine/threonine-specific protein kinase; protein kinase
complements SNF1 mutations in yeast
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; serine/threonine-specific protein kinase

Query Match
Best Local Similarity 22.0%; Score 367; DB 2; Length 512;
Matches 95; Conservative 47; Pred. No. 3.2e-11; Mismatches 113; Indels 16; Gaps 8;

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Qy    32 EPLESQYQVGPLLGSGGFPGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVV 91
Db    14 ESILPNYKLGKTLGISGFGKVKIAEHVVTGHKVAIKILNRRKIKN--MEMEEKVRREIK 70

Qy    92 LLKKVSSDFSGVIRLLDWFERPDSFVLILERPEEVQDLFDFITERGALQEDLARGFFWQV 151
Db    71 ILRLFMHPH--IIRQYEVIETTSDIYVVMEYVKS-GELFDYIVEKGRLQEDEARNFFQQI 127

Qy   152 LEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSSGALLKDTVYTDFD-GTRVYSPP 210
Db   128 ISGVEYCHRNMVVHRDLKPENLLD-SRCNIKIADFGLSNVMRDGHFLKTSCGSPNYAAP 186

Qy   211 EWIRYHRYRHGRSAAVWSLGILLLYDMVCGDIPFEHDEEI------IKGQVF-FRQTVSSEC 263
Db   187 EVISGKLYAGPEVDVWSCGVILYALLCGTLPFD-DENIPNLFKKIKGGIYTLPSHLSSEA 245

Qy   264 QHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
Db   246 RDLIPRMLIVDPVKRITIPEIRQHRWFQTHL 276
```

RESULT 15
S60304
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN12 (version 2) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 19-Mar-1997 #sequence_revision 15-Aug-1997 #text_change 05-Oct-2004
C;Accession: S60304; S24579
R;Halford, N.G.; Vicente-Carbajosa, J.; Sabelli, P.A.; Shewry, P.R.; Hannappel, U.; Krei
Plant J. 2, 791-797, 1992
A;Title: Molecular analyses of a barley multigene family homologous to the yeast protein
A;Reference number: S60303; MUID:93258420; PMID:1302632
A;Accession: S60304
A;Accesion: S60304
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-513 <HAL>
A;Cross-references: UNIPROT:Q40030; UNIPARC:UPI00001172C5D; EMBL:X65604
R;Halford, N.G.
submitted to the EMBL Data Library, April 1992
A;Reference number: S24579
A;Accession: S24579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61,'A',63-513 <HA2>
A;Cross-references: UNIPARC:UPI0000A3F6F; EMBL:X65604; NID:g18933; PIDN:CAA46554.1; PID
C;Superfamily: SNF1-related protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;15-272/Domain: protein kinase homology <KIN>
F;23-31/Region: protein kinase ATP-binding motif
F;46,65,143,145/Active site: Lys, Glu, Asp, Lys #status predicted
F;148,152/Binding site: magnesium (Asn, Asp) #status predicted
A;Cross-references: UNIPARC:UPI000017255D; EMBL:X65604
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

Query Match   21.6%;   Score 361; DB 1; Length 513;
Best Local Similarity   34.1%;   Pred. No. 6.2e-11;
Matches 94; Conservative 46; Mismatches 120; Indels 16; Gaps 8;

Qy   28 GKEKEPLESQYQVGPLLGSSGGFGSVYSGIRVADNLPVAIKHVEKDRISDWGELPNGTRVP 87
             |:|| : || :|:||.|| : |||::|||||||:|:| |||||:|| : |||
Db   8 GGHSEVLKN-YNLGKTLGLGTFGDVKVAERNVTGQRVAIKILNRRKMETMEMEEKGNR-- 64

Qy   88 MEVVLKKVSSDF--SGVIRLLDWFERPDSFVLILERPEPVQDLFDFITERGALQEDLAR 145
             : :: :|| | ||:||:|| : ||:::||:||:|||||:||||: :| ||||:||
Db   65 --EIKIMRLFIDFIHPHIIRVEVIETPKDIFVVMEYCNN-GELLDYIIENGRLQEDEAR 121

Qy   146 GFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRGEIKLIDFGSGALLKDTVYTDFD-GT 204
             | ||::| || |:|: ||:|||||||||| :::|::||:|||:.||:|||| || | :|
Db   122 RIFQQILAGVEYCHRIMVVHRDLKPENLLLD-SRYNVKLADFGLSNVWRDGHFLKTSCGS 180

Qy   205 RVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDIPFEHDE----EIIKGQVFFRQT- 258
             |:| | : |:|:|:| |:|||:|||:||||||: || ||| |||||.|::|:
Db   181 LNYAAPEIISSKLYAGPEVDVWSCGVVLYALLCGSVPFDDDNIPSLFRKIKGGTYILPSY 240

Qy   259 VSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDL 294
             | :|||:|::||:||| | | |:|||:||: :
Db   241 LSDSARDLIPKLLNIDPMKRITFHEIRVHPWFKNHL 276

Search completed: May 4, 2006, 05:25:51
Job time : 21.333 secs

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```
OM protein - protein search, using sw model

                                    GenCore version 5.1.7
                                    Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:               May  4, 2006, 05:12:40 ; Search time 122 Seconds
                                    (without alignments)
                                    1810.085 Million cell updates/sec

Title:    US-10-705-757-6
Perfect score:    1668
Sequence:    1 MLLSKINSLAHLRARPCNDL..........LLPQAASEIHLHSLSPGSSK 313

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:    2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:    2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 listing first 45 summaries

Database :    Uniprot_05.80:*
              1: uniprot_sprot:*
              2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES

Result                %
No.      Score    Query  Match  Length  DB  ID             Description
                  -------------------------------------------------------
  1      1668     100.0    313           1  P06803         mus musculu
  2      1662      99.6    313           2  Q8CFN8_MOUSE   mus musculu
  3      1584      95.1    313           1  PIM1_FELCA     felis silve
  4      1584      95.0    313           1  PIM1_RAT       rattus norv
  5      1582      94.8    313           1  PIM1_HUMAN     homo sapien
  6      1582      94.8    313           1  Q5TH7_HUMAN    homo sapien
  7      1574      94.4    313           1  PIM1_BOVIN     bos taurus
  8      1131      67.8    323           1  PIM3_COTJA     coturnix co
  9      1123.5    67.4    326           1  PPU85          bos taurus
 10      1123.5    67.3    326           1  PIM3_MOUSE     mus musculu
 11      1122.5    67.3    326           2  P58750         mus musculu
 12      1122.5    67.3    380           2  Q4VBM2_RAT     rattus norv
 13      1119      67.1    326           2  PIM3_HUMAN     homo sapien
 14      1113      66.7    323           2  PIM3_XENLA     xenopus lae
 15      1110      66.5    325           2  Q81X8_MOUSE    mus musculu
 16      1087      65.2    318           2  Q66Il1_XENTR   xenopus tro
 17      1080.5    64.8    337           2  Q5U489_XENLA   xenopus lae
 18      1056      63.3    316           2  Q4STF0_TETNG   tetraodon n
 19      861.5     51.6    311           2  Q8R2P0_MOUSE   mus musculu
 20      861.5     51.6    370           2  Q62070         mus musculu
 21      850       51.0    311           1  PIM2_HUMAN     homo sapien
 22      849       50.9    311           1  PIM2_MOUSE     mus musculu
 23      846       50.7    310           1  Q7ZVJ5_BRARE   brachydanio
 24      841       50.4    310           2  Q8JFW9_BRARE   brachydanio
 25      839       50.3    310           1  PIM1_BRARE     brachydanio
 26      787.5     47.2    288           2  Q9YhZ5_BRARE   brachydanio
 27      697.5     41.8    221           2  Q6D152_BRARE   brachydanio
 28      628       37.6    441           2  Q4TDC2_TETNG   tetraodon n
 29      624       37.4    500           2  Q8R120_MOUSE   mus musculu
 30      513       30.8    566           2  Q20443         caenorhabdi
 31      513       30.8    566           2  Q61JB7_CAEBR   caenorhabdi
 32      504       30.2    378           2  Q61JB7_CAEBR   caenorhabdi
 33      504       30.2    566           2  Q20443         caenorhabdi
     [continued]
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 32    443    26.6    270    2  Q5SPE4_BRARE   brachydanio
 33    425    25.5    465    2  Q5SPF6_BRARE   brachydanio
 34    419    25.1    416    2  Q4RFY6_TETNG   tetraodon n
 35    415.5  24.9    134    2  Q6P2J9_HUMAN   homo sapien
 36    400.5  24.0    268    2  Q5SPP9_BRARE   brachydanio
 37    400    24.0    281    2  Q5SV44_BRARE   brachydanio
 38    395    23.7   1383    1  PASK_MOUSE     mus musculu
 39    394    23.6    125    2  Q6Q2K5_CANFA   canis famil
 40    393    23.6    341    2  Q7PR39_ANOGA   anopheles g
 41    391.5  23.5    261    2  Q5SPP7_BRARE   brachydanio
 42    391.5  23.5    261    2  Q5SPQ2_BRARE   brachydanio
 43    388    23.3   1385    2  Q5PQT0_RAT     rattus norv
 44    385    23.1    463    2  Q5RG24_BRARE   brachydanio
 45    385    23.1    465    2  Q5RG26_BRARE   brachydanio
```

```
                                    ALIGNMENTS

RESULT 1
PIM1_MOUSE
ID   PIM1_MOUSE            STANDARD;      PRT;   313 AA.
AC   P06803;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20389540; PubMed=10931201;
RA   Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
RA   Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
RT   "PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
RL   Eur. J. Biochem. 267:5168-5178(2000).
RN   [2]
RT   "The primary structure of the putative oncogene pim-1 shows extensive
RT   homology with protein kinases.";
RL   Cell 46:603-611(1986).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9.
CC   -!- INTERACTION WITH RP9.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- DISEASE: Frequently activated by provirus insertion in murine
CC       leukemia virus-induced T-cell lymphomas.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
     -----------------------------------------------------------------------
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     between the Swiss Institute of Bioinformatics and the EMBL outstation -
     the European Bioinformatics Institute. There are no restrictions on its
     use as long as its content is in no way modified and this statement is not
     removed.
     -----------------------------------------------------------------------
DR   EMBL; M13945; AAA39930.1; -; Genomic_DNA.
DR   PIR; A24169; TVMSP1.
DR   HSSP; Q63450; 1A06.
SMR; P06803; 32-308.
DR   Ensembl; ENSMUSG00000024014; Mus musculus.
DR   MGI; MGI:97584; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
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DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167              Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
SQ   SEQUENCE   313 AA;  35537 MW;  79F4779E9DCBDC16 CRC64;

Query Match             100.0%;  Score 1668;  DB 1;  Length 313;
Best Local Similarity   100.0%;  Pred. No. 2.2e-115;
Matches  313;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180

Qy    181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300

Qy    301  EIHLHSLSPGSSK  313
           |||||||||||||
Db    301  EIHLHSLSPGSSK  313


RESULT 2
ID   Q8CFN8 MOUSE PRELIMINARY;    PRT;   313 AA.
AC   Q8CFN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Proviral integration site 1.
GN   Name=Pim1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL;  BC042885;  AAH42885.1;  -;  mRNA.
EMBL;  BC053019;  AAH53019.1;  -;  mRNA.
EMBL;  BC055316;  AAH55316.1;  -;  mRNA.
SMR;   Q8CFN8;  32-308.
Ensembl;  ENSMUSG00000024014;  Mus musculus.
MGI;  MGI:97584;  Pim1.
GO;  GO:0005524;  F:ATP binding;  IEA.
GO;  GO:0004674;  F:protein serine/threonine kinase activity;  IEA.
GO;  GO:0006468;  P:protein amino acid phosphorylation;  IEA.
InterPro;  IPR000719;  Prot_kinase.
InterPro;  IPR008271;  Ser_thr_pkin_AS.
InterPro;  IPR002290;  Ser_thr_pkinase.
Pfam;  PF00069;  Pkinase;  1.
ProDom;  PD000001;  Prot_kinase;  1.
SMART;  SM00220;  S_TKc;  1.
PROSITE;  PS00107;  PROTEIN_KINASE_ATP;  1.
PROSITE;  PS50011;  PROTEIN_KINASE_DOM;  1.
PROSITE;  PS00108;  PROTEIN_KINASE_ST;  1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA;  35451 MW;  1294F16A03B7C7D7 CRC64;

Query Match             99.6%;  Score 1662;  DB 2;  Length 313;
Best Local Similarity   99.7%;  Pred. No. 6.1e-115;
Matches  312;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD   60

Qy     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL  120

Qy    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG  180

Qy    181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI  240

Qy    241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS  300

Qy    301  EIHLHSLSPGSSK  313
           |||||||||||||
Db    301  EIHLHSLSPGSSK  313
```

RESULT 3
PIM1_FELCA
ID   PIM1_FELCA   STANDARD;   PRT;   313 AA.
AC   Q95LJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
RT   "The cDNA sequence of the feline pim-1 oncogene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; AB073748; BAB71752.1; -; mRNA.
DR   SMR; Q95LJ0; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35686 MW; C0BE268D633E6967 CRC64;

Query Match   95.0%; Score 1584; DB 1; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Mismatches 10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
         |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRTAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy 121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHICHNCGVLHRDIKDENLLIDL:RG 180
         ||||||||||||||||| ||||:|||:||||||||| ||||||||||||||||||||.||
Db 121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHICHNCGVLHRDIKDENLLIDLNRG 180

Qy 181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
         :|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy 241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
         ||||||| |||||||| ||||||||| ||| | ||||||||:|:|||:||| ||| :
Db 241 PFEHDEEIRQVFFRQRVSSECQHLIRWCLALRPSDRPSFEEIQNHPWMQDVLLPQETA 300

Qy 301 EIHLHSLSPGSSK 313
         |||||||||| ||
Db 301 EIHLHSLSPGPSK 313

RESULT 4
PIM1_RAT
ID   PIM1_RAT   STANDARD;   PRT;   313 AA.
AC   P26794;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=Pim1; Synonyms=Pim-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=92319652; PubMed=1620615;
RA   Wingett D., Reeves R., Magnuson N.S.;
RT   "Characterization of the testes-specific pim-1 transcript in rat.";
RL   Nucleic Acids Res. 20:3183-3189(1992).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---
DR   EMBL; X63675; CAA45214.1; -; mRNA.
DR   PIR; S26298; S26298.
DR   SMR; P26794; 32-308.
DR   Ensembl; ENSRNOG00000000529; Rattus norvegicus.
DR   RGD; 3330; Pim1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Kinase; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35631 MW; D575TDA9F1821BF9 CRC64;

Query Match   95.0%; Score 1584; DB 1; Length 313;
Best Local Similarity   94.2%;
Matches 295; Conservative   8; Mismatches 10; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60
         ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAPCNDLHANKLAPGKEKEPLESQYQVGPLLGSSGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

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Qy    121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILIDLSRG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db    121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNRG 180

Qy    181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy    241 PFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 PFEHDEEIVKGQVYFRQRVSSSECQHLIRWCLSLRPSDRPSFEEIQNHPWMQDVLLPQATA 300

Qy    301 EIHLHSLSPGGSSK 313
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Db    301 EIHLHSLSPSPSK 313
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RESULT 5

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ID   PIM1_HUMAN              STANDARD;      PRT;   313 AA.
AC   P11309; Q96RG3;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA   Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT   "Primary structure of the putative human oncogene, pim-1.";
RL   Gene 90:303-307(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA   Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT   "The cDNA sequence and gene analysis of the human pim oncogene.";
RL   Gene 54:105-111(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88217305; PubMed=3329709;
RA   Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA   Berns A.;
RT   "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT   and immunological identification of the in vitro synthesized PIM-1
RT   protein.";
RL   Oncogene Res. 1:103-112(1987).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 1-202.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [6]
RP   CHARACTERIZATION.
RX   MEDLINE=88266418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [7]
RP   FUNCTION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
RN   [8]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=22557470; PubMed=12680209;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA   Johnson T., Lilly M.B., Kraft A.S.;
RT   "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RT   localization is necessary for its biologic effects.";
RL   Anticancer Res. 23:167-178(2003).
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC       cells. May affect the structure or silencing of chromatin by
CC       phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC       hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html".
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; M27903; AAA60090.1; -; Genomic_DNA.
DR   EMBL; M16750; AAA60089.1; -; mRNA.
DR   EMBL; M54915; AAA36447.1; -; mRNA.
DR   EMBL; M24779; AAA81553.1; -; mRNA.
DR   EMBL; BC020224; AAH20224.1; -; mRNA.
DR   EMBL; AF386792; AAK70871.1; -; Genomic_DNA.
DR   PIR; JU0327; TVHUP1.
DR   PDB; 1XQZ; X-ray; A=14-313.
DR   PDB; 1XR1; X-ray; A=14-313.
DR   PDB; 1XWS; X-ray; A=1-313.
DR   PDB; 1YHS; X-ray; A=33-305.
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DR   PDB; 1YI3; X-ray; A=33-305.
DR   PDB; 1YI4; X-ray; A=33-305.
DR   PDB; 2BIK; X-ray; B=1-313.
DR   PDB; 2BIL; X-ray; B=1-313.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   HGNC; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   3D-structure; ATP-binding; Kinase; Nuclear protein;
KW   Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   BINDING      67     67       ATP (By similarity).
FT   CONFLICT     15     16       AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA;  35686 MW;  35BA76D366B69A3 CRC64;

Query Match             94.8%;  Score 1582;  DB 1;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 5.1e-109;
Matches  294;  Conservative   10;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
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Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLSRG 180
              |||||||||||||||||||||::|||:|||||||||||||||||||||||||||||:|||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy        181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||:|||||||:|||||||||:|||:||||||||:||||:|||||:|:|||| :
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGSSK 313
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Db        301 EIHLHSLSPGSSK 313

RESULT 6
ID   Q5T7H7_HUMAN    PRELIMINARY;      PRT;   313 AA.
AC   Q5T7H7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pim-1 oncogene (provial integration site 1).
GN   Name=PIM1; ORFNames=RP3-355M6.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
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RP   NUCLEOTIDE SEQUENCE.
RA   Laird G.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; AL353579; CAI20316.1; -; Genomic_DNA.
DR   SMR; Q5T7H7; 32-308.
DR   Ensembl; ENSG00000137193; Homo sapiens.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   313 AA;  35686 MW;  35BA76D366B69A3 CRC64;

Query Match             94.8%;  Score 1582;  DB 2;  Length 313;
Best Local Similarity   93.9%;  Pred. No. 5.1e-109;
Matches  294;  Conservative   10;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVAD 60
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| :
Db          1 MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQVGPLLGSGGFGSVYSGIRVSD 60

Qy         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFVLIL 120
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db         61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERPDSFVLIL 120

Qy        121 ERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLSRG 180
              |||||||||||||||||||||::|||:|||||||||||||||||||||||||||||:|||
Db        121 ERPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHNCGVLHRDIKDENLLIDLNRG 180

Qy        181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy        241 PFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||||:|||||||:|||||||||:|||:||||||||:||||:|||||:|:|||| :
Db        241 PFEHDEEIIRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy        301 EIHLHSLSPGSSK 313
              |||||||||||||
Db        301 EIHLHSLSPGSSK 313

RESULT 7
ID   PIM1_BOVIN     STANDARD;      PRT;   313 AA.
AC   Q9N0P9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21109090; PubMed=11182156; DOI=10.1016/S0165-2427(00)00259-2;
RA   Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
```

RT   "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL   Vet. Immunol. Immunopathol. 78:177-195(2001).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF250078; AAF67200.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   SMR; Q9NOP9; 32-308.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW   Phosphorylation; Proto-oncogene; Serine/threonine-protein kinase;
KW   Transferase.
FT   DOMAIN   38   290   Protein kinase.
FT   NP_BIND   44   52   ATP (By similarity).
FT   ACT_SITE   167   167   Proton acceptor (By similarity).
FT   BINDING   67   67   ATP (By similarity).
SQ   SEQUENCE   313 AA; 35630 MW; 9EF40229A847AD47 CRC64;

Query Match   94.4%; Score 1574; DB 1; Length 313;
Best Local Similarity   93.3%;
Matches 292; Conservative   12; Mismatches   9; Indels   0; Gaps   0;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAPGKEKEPLESQYVGPLLGSGGFGSVYSGIRVAD 60
              ||||||||||||||:||:|||||||||||||||||||||||||||||||||||||||||
Db   1 MLLSKINSLAHLRAAPCSDLHATKLAPGKEKEPLESQYVGPLLGSGGFGSVYSGIRVAD 60

Qy   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERDPSFVILL 120
              |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db   61 NLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSGFSGVIRLLDWFERDPSFVILL 120

Qy   121 EREPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCNCGVLHRDIKDENILIDLSRG 180
              ||||||||||||||||||||||:|||:||||||||||||||:|:|||||||||||||:||
Db   121 EREPEPVQDLFDFITERGALQEELARSFFWQVLEAVRHCHDCGVLHRDIKDENILIDLNRG 180

Qy   181 EIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCGDI 240
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ELKLIDFGSGALLKDTVVTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCGDI 240

Qy   241 PFEHDEEIIKGQVFFRQVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGDLLPQAAS 300
              |||||||:::|||||||:|||||||||:|||:||||||||:|||:||||:|:|||||:
Db   241 PFEHDEEIVRGQVFFRQRVSSECQHLIRWCLALRPSDRPTFEEIQNHPWMQDVLLPQETA 300

Qy   301 EIHLHSLSPGPSKK 313
              |||||||||||||
Db   301 EIHLHSLSPGPSK 313

RESULT 8
ID   PIM3_COTJA   STANDARD;   PRT;   323 AA.
AC   Q9PU85;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (qpim).
GN   Name=PIM3; Synonyms=PIM-3;
OS   Coturnix coturnix japonica (Japanese quail).

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;
RA   Eichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;
RT   "Developmental expression of Pim kinases suggests functions also
RT   outside of the hematopoietic system.";
RL   Oncogene 19:1215-1224(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AJ130845; CAB62386.1; -; mRNA.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   291   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   ACT_SITE   168   168   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   323 AA; 36597 MW; E2A4FA20B6F63996C CRC64;

Query Match   67.8%; Score 1131; DB 1; Length 323;
Best Local Similarity   67.1%;
Matches 208; Conservative   45; Mismatches   53; Indels   4; Gaps   3;

Qy   1 MLLSKINSLAHLRARPCNDLHATKLAP--GKEKEPLESQYVGPLLGSGGFGSVYSGIRV 58
              ||||| ||||| .   . :.| | || ||| ||||| ||:|||||| ||:||:|
Db   1 MLLSKFGSLAHICSPASMDHLPVKILPPVKVEKKPFDKYYQVGSVLGSGGFGTVYAGSRI 60

Qy   59 ADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERDPSFVL 118
              || ||||:||| |:   :||. : :.:::||:|||||||| . ||:||||:|| | |::
Db   61 ADGLPVAVKHVVKERVTEWGTI-GGVVMPLEIVLLKKVGSGFRGVIKLLDWYERPDGFLI 119

Qy   119 ILEREPEVQDLFDFITERGALQEDLARGFFWQVLEAVRHCNCGVLHRDIKDENILIDLS 178
              ::|||| |:|||||||:|||::|| :||||:||||||||| . ||:|||||||:|:||:
Db   120 VMEREPLVKDLFDFITEKGALDEDTARGFFRQVLEAVRHCYGCGVVHRDIKDENLLVDLR 179

Qy   179 RGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLLYDMVCG 238
              .|| ||||||||||||||||||||||||||||||||||||||||:|||||:||:||||||
Db   180 TGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLIYDMVCG 239

Qy   239 DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM-QGDLLPQ 297
              |||||:|||::.|:::|| .| ||||:|||||||||||||||::|:::|.|| . ::.
Db   240 DIPFEQDEEILRGRLYFRRRISPECQQLIKWCLSLRPSDRPTLEQIFDHQWMHKSEVVKS 299

Qy   298 AASEIHLHSL 307
               .:|:.|..|
Db   300 EDCDIRLRTL 309

RESULT 9
ID   PIM3_MOUSE   STANDARD;   PRT;   326 AA.

AC   P58750;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=Pim3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=FVB/N; TISSUE=Colon, and salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; BC017621; AAH17621.1; -; mRNA.
DR   EMBL; BC026639; AAH26639.1; -; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   Ensembl; ENSMUSG00000035828; Mus musculus.
DR   MGI; MGI:1355297; Pim3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser/Thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN   40   293   Protein kinase.
FT   NP_BIND   46   54   ATP (By similarity).
FT   BINDING   170   170   ATP (By similarity).
FT   ACT_SITE   169   169   Proton acceptor (By similarity).
FT   BINDING   69   69   ATP (By similarity).
SQ   SEQUENCE   326 AA; 35970 MW; DD68CBF46354851E CRC64;

Query Match   67.4%; Score 1123.5; DB 1; Length 326;
Best Local Similarity   71.0%;
Matches 213; Conservative 31; Mismatches 43; Indels 13; Gaps   5;

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Qy          1 MLLSKINSLAHLRARPC------NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
                |||||  |||||| ||        :||| ||| | | :| |||: :||| ||||||||:
```

Db   1 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYA 56

Qy   55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
Db   57 GSRIADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLRKVGAGGARGVIRLLDWFER 115

Qy   113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
Db   116 PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVHRDIKDEN 175

Qy   173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
Db   176 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 235

Qy   233 YDMVCGDIPFEHDEEIIKQVFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
Db   236 YDMVCGDIPFEQDEEILKGRGLFFRRRVSPECQQLIEWCLSLRPSERPSLDQIAAHPWMLG 295

RESULT 10
PIM3_RAT
ID   PIM3_RAT   STANDARD;   PRT;   326 AA.
AC   O70444;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Protein kinase
DE   Kid-1) (Kinase induced by depolarization).
GN   Name=Pim3; Synonyms=Kid1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Konietzko U., Kuhl D.;
RT   "Pim-3 is a member of the pim kinase family.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RX   MEDLINE=98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
RA   Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,
RA   Bazan N.G., Baudry M., Herschman H.R.;
RT   "KID-1, a protein kinase induced by depolarization in brain.";
RL   J. Biol. Chem. 273:16535-16543(1998).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues,
CC   including brain.
CC   -!- INDUCTION: By membrane depolarization or forskolin.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC   subfamily.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF086224; AAC68900.1; ALT_INIT; mRNA.
DR   EMBL; AF057026; AAC36065.1; -; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   RGD; 620462; Pim3.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR   GO; GO:0004672; F:protein kinase activity; IDA.
DR   GO; GO:0046777; P:autophosphorylation; IDA.
DR   GO; GO:0016572; P:histone phosphorylation; IDA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_Thr_pkin_AS.
DR   InterPro; IPR002290; Ser/Thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.

```
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       40    293       Protein kinase.
FT   NP_BIND      46     54       ATP (By similarity).
FT   ACT_SITE    170    170       Proton acceptor (By similarity).
FT   BINDING      69     69       ATP (By similarity).
SQ   SEQUENCE   326 AA;  36002 MW;  DD6C9BF4635F851E CRC64;

Query Match             67.3%;  Score 1122.5;  DB 1;  Length 326;
  Best Local Similarity   71.0%;  Pred. No. 5.7e-75;
  Matches  213;  Conservative   31;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
              ||||  |||||       |  : ||  | ||   :|:|||||||| ||||||||| ||:
Db          1 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKYYQVGAVLGSGGFGTVYA 56

Qy         55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
              | |||| |||||||| ||  |  | : |  |: ||:||||||  ||| ||||||||||||
Db         57 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 115

Qy        113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
              || |:|:|||||| ||||||||||||:| |||| || |||| |||||||||:|||||||
Db        116 PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 175

Qy        173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
              :|:||| ||:|||||||||:||||||||||||||||||||||||||||||:||||| ||
Db        176 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 235

Qy        233 YDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
              ||||||||||:|||| : |::|   |||| || |::|||||||::||| :: |:|||| |
Db        236 YDMVCGDIPFEQDEEILRGRLFPRRRVSPECCQQLIEWCLSLRPSERPSLDQIAAHPWMLG 295
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RESULT 11

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ID   Q4V8M2_RAT     PRELIMINARY;      PRT;   380 AA.
AC   Q4V8M2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; BC097317; AAH97317.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
FT   NON_TER       1      1
SQ   SEQUENCE   380 AA;  41568 MW;  F82BEB85D0D71346 CRC64;

Query Match             67.3%;  Score 1122.5;  DB 2;  Length 380;
  Best Local Similarity   71.0%;  Pred. No. 6.9e-75;
  Matches  213;  Conservative   31;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          1 MLLSKINSLAHLRARPC-----NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS 54
              ||||  |||||       |  : ||  | ||   :|:|||||||| ||||||||| ||:
Db         55 MLLSKFGSLAHL----CGPGGVDHLPVKILQPAKADKESFEKYYQVGAVLGSGGFGTVYA 110

Qy         55 GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER 112
              | |||| |||||||| ||  |  | : |  |: ||:||||||  ||| ||||||||||||
Db        111 GSRIADGLPVAVKHVVKERVTEWGSL-GGMAVPLEVVLLRKVGAAGGARGVIRLLDWFER 169

Qy        113 PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN 172
              || |:|:|||||| ||||||||||||:| |||| || |||| |||||||||:|||||||
Db        170 PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN 229

Qy        173 ILIDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL 232
              :|:||| ||:|||||||||:||||||||||||||||||||||||||||||:||||| ||
Db        230 LIVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL 289

Qy        233 YDMVCGDIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQG 292
              ||||||||||:|||| : |::|   |||| || |::|||||||::||| :: |:|||| |
Db        290 YDMVCGDIPFEQDEEILRGRLFPRRRVSPECCQQLIEWCLSLRPSERPSLDQIAAHPWMLG 349
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RESULT 12

```
ID   PIM3_HUMAN     STANDARD;      PRT;   326 AA.
AC   Q86V86; Q68BM2;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
GN   Name=PIM3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Liver;
RX   PubMed=15542001; DOI=10.1002/ijc.20719;
RA   Fujii C., Nakamoto Y., Lu P., Tsuneyama K., Popivanova B.K.,
RA   Kaneko S., Mukaida N.;
RT   "Aberrant expression of serine/threonine kinase Pim-3 in
RT   hepatocellular carcinoma development and its role in the proliferation
RT   of human hepatoma cell lines.";
RL   Int. J. Cancer 114:209-218(2005).
```

```
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   IDENTIFICATION FROM ESTS.
RX   MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;
RA   Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.;
RT   "Consistency checks for characterizing protein forms.";
RL   Comput. Biol. Chem. 27:29-35(2003).
CC   -!- FUNCTION: May be involved in cell cycle progression and anti-
CC       apoptosis process. Implicated in proliferation of human hepatoma
CC       cell lines.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: Widely expressed. No expression in colon,
CC       thymus, and small intestine. Expressed in human hepatoma cell
CC       lines but not in normal liver tissues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   --------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------
DR   EMBL; AB114795; BAD42438.1; -; mRNA.
DR   EMBL; BC052239; -; NOT_ANNOTATED_CDS; mRNA.
DR   Ensembl; ENSG00000198355; Homo sapiens.
DR   HGNC; HGNC:19310; PIM3.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN        40    293       Protein kinase.
FT   NP_BIND       46     54       ATP (By similarity).
FT   ACT_SITE     170    170       Proton acceptor (By similarity).
FT   BINDING       69     69       ATP (By similarity).
SQ   SEQUENCE   326 AA;  35863 MW;  41FDF9DD2467A162 CRC64;
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Query Match             67.1%;  Score 1119;  DB 1;  Length 326;
Best Local Similarity   67.9%;
Matches  216;  Conservative  35;  Mismatches  53;  Indels  14;  Gaps   6;

Qy        1  MILSKINSLAHLRARPC------NDLHATKLAPGK-EKEPLESQYQVGPLLGSGGFGSVYS   54
             |||||  ||| |||||||      ||...||||| |||||||.||||||..||||||:|
Db        1  MLLSKFGSLAHL---------CGPGGVDHLPVKILQPAKADKESFEKAYQVGAVLGSGGFGTVYA   56

Qy       55  GIRVADNLPVAIKHIVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER   112
             |.|...|||:|||  | ::||     |:||||||:::|||      ::|||:||||||||
Db       57  GSRIADGLPVAVGKHVVKERVTEWGSL-CGATVPLEVVLLRKVGAAGGARGVIRLLDWFER   115

Qy      113  PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCINCGVLHRDIKDEN   172
             || ||:|:|||||.|||||||||||||: : ||| || ||:||||| .|||:||||||||
Db      116  PDGFLVLLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHSCGVVHRDIKDEN   175

Qy      173  ILILDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL   232
             :|: || :||:|||||||||||||||||||||||||||||||||||||||||: |||| |||
Db      176  LIVDLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATWSLGVLL   235

Qy      233  YDMVCGDIPFEHDEEIIKGQVFRQTVSSECHLIKWCLSLRPSDRPSFEEIRNHPWMQG   292
             |||:|||||||:||||: | : ||| |||: :|:|||||||:|||:::||  |||| |
Db      236  YDMWCGDIPFEQDEEILGRLLFRRVSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLG   295

Qy      293  -DLLPQAASEIHLHSLSP   309
              | || ||| :| |:|
Db      296  ADGGAPESCDLRLCTLDP   313
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RESULT 13
PIM3_XENLA
ID   PIM3_XENLA     STANDARD;     PRT;   323 AA.
AC   Q91BZ2;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37) (Pim-1).
GN   Name=PIM3; Synonyms=PIM1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, AND PHOSPHORYLATION SITES.
RX   MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
RA   Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.,
RA   Aebersold R., Pelech S.L.;
RT   "Identification of the autophosphorylation sites of the Xenopus laevis
RT   Pim-1 proto-oncogene-encoded protein kinase.";
RL   J. Biol. Chem. 272:10514-10521(1997).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- PTM: Autophosphorylated.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- CAUTION: Was originally (Ref.1) called Pim-1 but seems to
CC       represent the pim-3 isoform.
CC   --------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------
DR   EMBL; L29495; AAA85389.1; -; mRNA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN        40    291       Protein kinase.
FT   NP_BIND       46     54       ATP (By similarity).
FT   ACT_SITE     168    168       Proton acceptor (By similarity).
FT   BINDING       69     69       ATP (By similarity).
FT   MOD_RES        4      4       Phosphoserine (partial).
FT   MOD_RES      190    190       Phosphoserine (by autocatalysis).
FT   MOD_RES      190    190       Phosphoserine (by autocatalysis).
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FT   MOD_RES    205   205   Phosphothreonine (by autocatalysis)
FT   SEQUENCE   323 AA;  36964 MW;  AB4DD61E7A99A38F CRC64;
SQ

Query Match   Best Local Similarity   66.7%;   Score 1113;  DB 1;  Length 323;
                         65.8%;   Pred. No. 2.9e-74;
Matches 208;  Conservative 46;  Mismatches 56;  Indels 6;  Gaps 5;

Qy    1  MLLSKINSLAHLRARPCNDLH--ATKLAPGK-EKEPLESQYQVGPLLGGSGGFGSVYS   54
         |||||:||| ||::  :  :||    ||||   ||||| ||||:||:: | ||||||||
Db    1  MLLSKFGSLAHI-CNPSNMEHLPVKILQPVKVDKEPFEKVYQVGSVVASGGFGTVYSDSR  59

Qy   58  VADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLDWFERPDSFV  117
         :||:|||||||||||:|||||||||||||||||||||||| |||||||||||||||||:
Db   60  IADQVPVAVKHVAKERVTEWGTL-NGVMVPLEIVLLKKVPTAFRGVINLLDWYERPDAFL  118

Qy  118  LILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDENILLDL  177
         |||||||||||||||||||||||||||||||||||||||||||||||||:||||| ||:
Db  119  IVWERPEPVKDLFDYITEKGPLDEDTARGFFRQVLEAVRHCYNCGVVHRDIKDENLLVDT  178

Qy  178  SRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVC  237
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Db  179  RNGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLLYDMVY  238

Qy  238  GDIPFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM-QGDLLP  296
         ||||||||||||||||||||| |||||||||||||||||||||| |:|||:|||| |||||
Db  239  GDIPFEQDEEIVRLCFRRRISTECQQLIKWCLSLRPSDRPTLEQIFDHPWMCKCDLVK    298

Qy  297  QAASEIHLHSLSPGSS   312
         : ||||||||||||||
Db  299  SEDCDLRTIDNDSS      314
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RESULT 14
ID   Q811X8_MOUSE   Q811X8_MOUSE PRELIMINARY;   PRT;   325 AA.
AC   Q811X8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Kid1.
GN   Name=Pim3; Synonyms=Kid1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yu L.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AY026339; AAK16606.1; -; mRNA.
HSSP; Q03656; 1Q99.
SMR; Q811X8; 36-292.
MGI; MGI:1355297; Pim3.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_Thr_pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   325 AA;  35931 MW;  77DEF8B20F41E3F4 CRC64;

Query Match   Best Local Similarity   66.5%;   Score 1110;  DB 2;  Length 325;
                         70.7%;   Pred. No. 4.8e-74;
Matches 212;  Conservative 32;  Mismatches 42;  Indels 14;  Gaps 6;
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```
RESULT 15
ID   Q6III1_XENTR   Q6III1_XENTR PRELIMINARY;   PRT;   318 AA.
AC   Q6III1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Pim3-prov protein.
GN   Name=pim3-prov;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC081340; AAH81340.1; -; mRNA.
SMR; Q6III1; 32-297.
Ensembl; ENSXETG00000009354; Xenopus tropicalis.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
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Qy    1  MLLSKINSLAHLRARPC------NDLHATKLAPGK-EKEPLESQYQVGPLLGGSGGFGSVYS   54
         |||||  ||||| ||          | |  |||||  ||||| ||||||  |  |||||: :
Db    1  MLLSKFGSLAHL----CGPGVDHLPVKILQPAKADKESFEKVYQVGAVLGSGGFGTVYA    56

Qy   55  GIRVADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKV--SSDFSGVIRLLDWFER  112
         |  : |:||||:|||:| | : || :|:|| || : :||| | ||:| ||||  |||||
Db   57  GSRIADGLPVAVKHVVKERVTEWGSL-GGVAVPLEVVLLRKVGAAGGARGVIRLLDWFER  115

Qy  113  PDSFVLILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNCGVLHRDIKDEN  172
         |   | ||| |||||||||||||||||||||||||||||||||||||||| |||||||||
Db  116  PDGFLLVLERPEPAQDLFDFITERGALDEPLARRFFAQVLAAVRHCHNCGVVHRDIKDEN  175

Qy  173  ILDLSRGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILL  232
         || | |||||||||||||| |||||||||||||||||||||||||||||||||||| ||
Db  176  LLVDLRSGELKLIDFGSGAVLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSATVWSLGVLL  235

Qy  233  YDMVCGDIPFEHDEEIIKGQVFFRQTVSSSECQHLIKWCLSLRPSDRPSFEEIRNHPWM   292
         ||||||||||||||| || || || || | |  || |||||||||  ||  |   |||
Db  236  YDMVCGDIPFEQDEEILRGRLFPRRRVSPECQQLIEWCLSLRPSERPSLDKL-CHPWMLG  294
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DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Cell cycle; Cell division; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   318 AA;  36547 MW;  48CCF12797F01FDC CRC64;

Query Match            65.2%;  Score 1087;  DB 2;  Length 318;
Best Local Similarity  67.1%;  Pred. No. 2.4e-72;
Matches  198; Conservative  42; Mismatches  47;  Indels   8;  Gaps   3;

Qy      3 LSKINSLAHLRARPCNDLHATKLAPGKE----KEPLESQYQVGPLLGSGGFGSVYSGIRV   58
            :||:|.:|---|.:|  :|::|||||||||:|:||||:|::|||:|:
Db      1 MSSVQVIYH---QKIHNYHLNSVFPKDDLPAVKEPFENCYQGPVIGTGGFGTVYSGVRI   57

Qy     59 ADNLPVAIKHVEKDRISDWGELPNGTRVPMEVVLLKKVSSDFSGVIRLLLDWFEBRPDSFVL  118
           :||:|.::|||:|.|||:|:|.| :|.:|::| |::|| ||.||.|||||||||||:|
Db     58 SDKLPVAIKHVSRDRIGEMKDHM-NGTLVPLEIYLLKKVSNGCRGVIRLLLDDWYERPDGFII  116

Qy    119 ILERPEPVQDLFDFITERGALQEDLARGFFWQVLEAVRHCHNGGVLHRDIKDENILIDLS  178
           :||||||||||||||||||| |: ||||||||:||||||||||||||||:|||::||:||
Db    117 IMERPEPVQDLFDFITERGALGEELATNFFRQVVEAVRHCHSCDVVHRDIKDENILVDLR  176

Qy    179 RGEIKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRYHRYHGRSAAVWSLGILLYDMVCG  238
           |:|||||||||||||:||||||||||||:|||||||:||.|||||.||||||||||||||
Db    177 TAELKLIDFGSGALLRDAVYTDFDGTRVYSPPEWIRFHKYHGRSATVWSLGILLYDMVCG  236

Qy    239 DIPFEHDEEIIKGQVFFRQTVSSECQHLIKWCLSLRPSDRPSFEEIRNHPWMQGD  293
           |||||||||:|||:||.|.|::|||||||||||||:|||||||||||||:||||||
Db    237 DIPFEHDDEILKGKIQYRCVRSRECQHLIEWCLSKRPSDRPSLEQILAHPWMSQD  291

Search completed: May 4, 2006, 05:18:58
Job time : 123 secs
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